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OM protein - protein search, using SW model

Run on: December 2, 2004, 22:07:09 / Search time 162 Seconds
(without alignments)
1643.069 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858
Sequence: 1 MADSSBGPAPGAEVAAELPG.....GQVSKSKHIMLQSGRRRL 742

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003s:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	4	AAE06683 Human van
2	3829	99.2	831	8	AD181606 Human van
3	3829	99.2	871	4	AAE01227 Human van
4	3829	99.2	871	4	AAE01227 Human van
5	3829	99.2	871	5	AAE01227 Human van
6	3829	99.2	871	5	AAE01227 Human van
7	3829	99.2	871	5	AAE01227 Human van
8	3829	99.2	871	5	AAE01227 Human van
9	3829	99.2	871	5	AAE01227 Human van
10	3829	99.2	871	5	AAE01227 Human van
11	3829	99.2	871	5	AAE01227 Human van
12	3829	99.2	871	5	AAE01227 Human van
13	3829	99.2	871	5	AAE01227 Human van
14	3829	99.2	871	5	AAE01227 Human van
15	3829	99.2	871	5	AAE01227 Human van
16	3829	99.2	871	5	AAE01227 Human van
17	3829	99.2	871	5	AAE01227 Human van
18	3829	99.2	871	5	AAE01227 Human van
19	3829	99.2	871	5	AAE01227 Human van
20	3829	99.2	871	5	AAE01227 Human van
21	3829	99.2	871	5	AAE01227 Human van
22	3829	99.2	871	5	AAE01227 Human van
23	3829	99.2	871	5	AAE01227 Human van
24	3829	99.2	871	5	AAE01227 Human van
25	3829	99.2	871	5	AAE01227 Human van

26	3689	95.6	871	8	AD181610 Mouse OTR
27	3685	95.5	871	7	AD332559 Murine TR
28	3681	95.4	871	4	AAE07209 Amino aci
29	3636	94.2	873	8	AD181594 Mouse van
30	3472	90.0	803	8	AD181586 Human van
31	3470	89.9	811	4	AAE06682 Human van
32	3467	89.9	803	4	AAE063208 Amino aci
33	3389	87.8	803	8	AD181592 Mouse van
34	3284	85.1	852	8	AD181566 Chicken v
35	3120	80.9	743	4	AAE03209 Amino aci
36	2373.5	61.5	602	5	AAU74936 Amino aci
37	2315.5	60.0	1115	4	ABG28242 Novel hum
38	2156.5	55.9	559	5	AAE16773 Human tra
39	1808	46.9	498	4	AAE04889 Human tra
40	1604.5	41.6	843	2	AAE06561 Chicken C
41	1601.5	41.5	843	2	AAW97979 Chicken C
42	1580.5	41.0	838	8	AD181568 Rat vanil
43	1579.5	40.9	838	2	AAE06555 Rat capsa
44	1579.5	40.9	838	2	AAW97979 Rat VRL C
45	1579.5	40.9	838	4	AAE01228 Rattus va

ALIGNMENTS

RESULT 1	AAE06683	standard; protein; 742 AA.
ID	AAE06683	
XX	AAE06683;	
AC	16-OCT-2001	(first entry)
DT	16-OCT-2001	(first entry)
XX		
DE	Human vanilloid receptor VR3 isoform, VR3A+B+.	
KW	Human, vanilloid receptor; VR3; inflammatory condition; analgesic;	
KW	intracranial pain; postherpetic neuralgia; diabetic neuropathy; asthma;	
KW	postmastectomy pain; complex regional pain syndrome; arthritis;	
KW	rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;	
KW	chronic obstructive pulmonary disease; irritable bowel syndrome;	
KW	psoriasis; central nervous system disease; CNS; cancer;	
KW	intestinal tract disorder; VR3A+B+.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200158945-A1.	
PD	16-AUG-2001.	
XX		
PF	01-FEB-2001; 2001WO-US003456.	
XX		
PR	08-FEB-2000; 2000US-00500123.	
XX		
PA	(ORTH) ORTHO-MCNEIL PHARM INC.	
PI	Dubin AB, Huvor A, Glass CA, Exlander MG;	
XX	WPI: 2001-488969/53.	
DR	N-PBDB; AAD12793.	
XX		
PT	New human VR3 receptor useful for the treatment of disorders including	
XX	cancers arthritis and pain.	
PS	Claim 11; Fig 8; 104pp; English.	
XX		
CC	The patent relates to human vanilloid receptor VR3 polynucleotide and	
CC	polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B+	
CC	have also been disclosed. The VR3 polypeptide is used to identify its	
CC	modulators which are useful for the treatment of inflammatory conditions	
CC	and for use as analgesics for intractable pain associated with	
CC	postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex	
CC	regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),	
CC	as well as ulcers, neurodegenerative diseases, asthma, chronic	

CC obstructive pulmonary disease, irritable bowel syndrome and psoriasis.
 CC The VR3 modulators are also useful for treatment of central nervous
 CC system (CNS) diseases, diseases of the intestinal tract, abnormal
 CC proliferation and cancer. The present sequence is human VR3 receptor
 CC isoform, VR3A+B+

CC Sequence 742 AA;

Query Match 100.0%; Score 3858; DB 4; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGEVAVELPGDESGTGGRAFLPSLIANLFEGBDGLSPSPADASHPAP 60
 DB 1 MADSSGPRAGGEVAVELPGDESGTGGRAFLPSLIANLFEGBDGLSPSPADASHPAP 60
 QY 61 GGRPMLRMKFOGAFKGVNPIIDLLESTLYESSVPGKKA PMDSLFTYGYRRHSSDN 120
 DB 61 GGRPMLRMKFOGAFKGVNPIIDLLESTLYESSVPGKKA PMDSLFTYGYRRHSSDN 120
 QY 121 KEMRKTIIEKOPSPKAPAPPPILKVNRPILFDIVRGSTADHDGLLPILTEKKRL 180
 DB 121 KEMRKTIIEKOPSPKAPAPPPILKVNRPILFDIVRGSTADHDGLLPILTEKKRL 180
 QY 181 TDEEFEPSTGKTCLEPKALLNSGRNDTIPVLLDIAERTGNMKEPINSPPFDIYRGQT 240
 DB 181 TDEEFEPSTGKTCLEPKALLNSGRNDTIPVLLDIAERTGNMKEPINSPPFDIYRGQT 240
 QY 241 ALHIAIERCKHVELLVAGADVAHQARGFPQPDGEGYFFKGLPLSLA CTNPHI 300
 DB 241 ALHIAIERCKHVELLVAGADVAHQARGFPQPDGEGYFFKGLPLSLA CTNPHI 300
 QY 301 VAVLTENPKKADMRQDSRGNTVLAHVLAADNTRENTKFTVKKMYDLILKCARLPDS 360
 DB 301 VAVLTENPKKADMRQDSRGNTVLAHVLAADNTRENTKFTVKKMYDLILKCARLPDS 360
 QY 361 NLEAVLNNDGLSPLMAAAKTGKIGIFOHIIIRREVTDETRHLSRKPKDVA YGVSYLYD 420
 DB 361 NLEAVLNNDGLSPLMAAAKTGKIGIFOHIIIRREVTDETRHLSRKPKDVA YGVSYLYD 420
 QY 421 LLSLDTCGEBASVLEILVYNSKIENRHEMLAVEPINELLDDKRRKGAVSFYINVS YLC 480
 DB 421 LLSLDTCGEBASVLEILVYNSKIENRHEMLAVEPINELLDDKRRKGAVSFYINVS YLC 480
 QY 481 AMVIFTLTAYOPELGPYPYPTVDYLRAGSVITLFTGVLPFFTNIDLMFKKCPGV 540
 DB 481 AMVIFTLTAYOPELGPYPYPTVDYLRAGSVITLFTGVLPFFTNIDLMFKKCPGV 540
 QY 541 NSLFDIGSPQLLYFYSVLVIVSALVLAGIEAVLAVMFALVIGMNNALYFRGLKLTG 600
 DB 541 NSLFDIGSPQLLYFYSVLVIVSALVLAGIEAVLAVMFALVIGMNNALYFRGLKLTG 600
 QY 601 TYSIMTOKILFKLFRFLVYLLFMGYASALVSLNPCNNMVCNDQNCVPTVPSG 660
 DB 601 TYSIMTOKILFKLFRFLVYLLFMGYASALVSLNPCNNMVCNDQNCVPTVPSG 660
 QY 661 RDSSTFTFLDLFKLTIGKDELMSTKYPVFIILVTYIILFVLLNMLALMGE 720
 DB 661 RDSSTFTFLDLFKLTIGKDELMSTKYPVFIILVTYIILFVLLNMLALMGE 720
 QY 721 TVGVSKESHIMWLGSGRRRL 742
 DB 721 TVGVSKESHIMWLGSGRRRL 742

RESULT 2

ID AD181606 standard; protein; 831 AA.

XX AC AD181606;

XX DT 22-APR-2004 (first entry)

DE Human vanilloid receptor-related channel protein #2.

XX Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.

OS Homo sapiens.

PN US2004009537-A1.

PD 15-JAN-2004.

PF 13-JAN-2003; 2003US-00342844.

PR 11-JAN-2002; 2002US-0347459P.

PR 02-AUG-2002; 2002US-0401171P.

PR 20-AUG-2002; 2002US-0405678P.

PA (ROOS/) ROOS J.

PA (STAU/) STAUDERMAN K.

PA (VEL/) VELICELEBI G.

PI Roos J, Stauderman K, Velicelebi G;

XX MPI; 2004-090465/09.

XX N-PSDB; AD181605.

PS Disclosure; SEQ ID NO 76; 55pp; English.

XX The invention relates to identifying an agent that modulates

XX intracellular calcium comprising monitoring the effects of the agent on

XX store-operated calcium entry comprising contacting one or more test cells

XX or their portion comprising one or more proteins that is (are) at least

XX about 35% homologous to the protein encoded by Drosophila gene CG4536 or

XX CG5842 over at least about 40% of the encoded protein (and that provides

XX for store-operated calcium entry with a test agent), where the portion of

XX the cell comprises the proteins, monitoring the effect(s) of the test

XX compound on store-operated calcium entry and identifying a test agent as

XX an agent if it has an effect on store-operated calcium entry. Also

XX included are a method of modulating store-operated calcium entry

XX (comprising modulating the level of, expression of, activity of or

XX molecular interactions of a protein in a cell that has altered store-

XX operated calcium entry, where the protein is at least about 35%

XX homologous to the protein encoded by Drosophila gene CG4536 or CG5842

XX over at least about 40% of the encoded protein and that provides for

XX store-operated calcium entry, and where store-operated calcium transport

XX into the cell is modulated) and a method of identifying a molecule that

XX provides for store-operated calcium entry (comprising identifying a

XX molecule that interacts with the protein mentioned above, thus,

XX identifying molecules involved in modulating store-operated calcium

XX entry. The protein does not contain the contiguous sequences appearing as
 CC AD181644 and AD181645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g. glomerulonephritis).
 CC The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.

XX Sequence 831 AA;

Query Match 99.2%; Score 3829; DB 8; Length 831;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MADSEGRAGGEVAELPGESGTPGGEAFLPLSLANLPEFGEGSLSPSPADASRPAGP	60
Db	1	MADSEGRAGGEVAELPGESGTPGGEAFLPLSLANLPEFGEGSLSPSPADASRPAGP	60
QY	61	GDGRPNLIMKFGQAFRRKGVNPIDLLESTLYESSVVPQPKAPMDSLFDYGTYYHHSSDN	120
Db	61	GDGRPNLIMKFGQAFRRKGVNPIDLLESTLYESSVVPQPKAPMDSLFDYGTYYHHSSDN	120
QY	121	KRMKKIKIEKQPSQKAPAPQPPILKVFNNPILFDIYRSGSTADLDGLPEFLTHKKRL	180
Db	121	KRMKKIKIEKQPSQKAPAPQPPILKVFNNPILFDIYRSGSTADLDGLPEFLTHKKRL	180
QY	161	TDEFFRSTGTCTCLPKALLNSGRDPTVLLDIAERTGNMEEFINSPPRIDYYRGQT	240
Db	161	TDEFFRSTGTCTCLPKALLNSGRDPTVLLDIAERTGNMEEFINSPPRIDYYRGQT	240
QY	241	ALHAIERRCKHYVELLVAQADVAHAARGFPQPKQEGGYFGEPLSLAAGTNPPI	300
Db	241	ALHAIERRCKHYVELLVAQADVAHAARGFPQPKQEGGYFGEPLSLAAGTNPPI	300
QY	301	VNVLTPNPKKADMRDSDRGNTVLAHLVALADTRENKFTVPMQYLLILKKARLPDS	360
Db	301	VNVLTPNPKKADMRDSDRGNTVLAHLVALADTRENKFTVPMQYLLILKKARLPDS	360
QY	361	NLEAVLNNDGLSPILMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDMAVGYVSSLYD	420
Db	361	NLEAVLNNDGLSPILMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDMAVGYVSSLYD	420
QY	421	LSSLDTCGEASVLEILVYNSKLENREMLAVEPINELRDYKRKGANVYINNVSYLC	480
Db	421	LSSLDTCGEASVLEILVYNSKLENREMLAVEPINELRDYKRKGANVYINNVSYLC	480
QY	481	AMVIFLLTAYOPELGGTPPYRPTVDYTLAGEVITLFTGVLPFTNTIKDLFMKKCPGV	540
Db	481	AMVIFLLTAYOPELGGTPPYRPTVDYTLAGEVITLFTGVLPFTNTIKDLFMKKCPGV	540
QY	541	NSLPIFGSFOILYFIYSVLVYSAALYLAGIEBAYLAVMFPALVGMNNALYFTRGILKG	600
Db	541	NSLPIFGSFOILYFIYSVLVYSAALYLAGIEBAYLAVMFPALVGMNNALYFTRGILKG	600
QY	601	TVSIMGKILFKDLFRFLVYLLFPMGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC	660
Db	601	TVSIMGKILFKDLFRFLVYLLFPMGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC	660
QY	661	RQSEETSTFLDLFKLTIGMDLEMSRKYPVFIIILVYIILFENLIMLALMGE	720
Db	661	RQSEETSTFLDLFKLTIGMDLEMSRKYPVFIIILVYIILFENLIMLALMGE	720
QY	721	TVGQVSKESKHIMKLG 736	
Db	721	TVGQVSKESKHIMKLG 736	
RESULT 3			
AAE01227			
ID	AAE01227	standard; protein; 871 AA.	
XX	AAE01227;		
AC			
XX			
DT	31-JUL-2001	(first entry)	
XX			
DE		Human vanilloid receptor 3 (hVR3) protein.	
XX			
KW		Human; vanilloid receptor 3; VR3; inflammation; arthritis; psoriasis;	
KW		wound healing; analgesic; vulnary; anti-allergic; gene therapy;	
KW		neuropathic pain; rhinitis; pruritus; bladder dysfunction;	
XX		cluster headache; capsaicin-sensitive ion channel disorder.	
OS		Homo sapiens.	
XX			
EH	Key	Location/Qualifiers	
FT	Domain	238..269	
FT		/label= Ankaryn repeat	

Query Match	Best Local Similarity	99.2%: Score 3829;	DB 4;	Length 871;
Matches 736;	Conservative 100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;
			Gaps 0.0;	
FT	Domain	284. .316		
FT	/label= Ankaryn_repeat			
FT	Domain	369. .402		
FT	/label= Ankaryn_repeat			
FT	Domain	470. .491		
FT	/label= Transmembrane_domain			
FT	Domain	515. .535		
FT	/label= Transmembrane_domain			
FT	Domain	551. .570		
FT	/label= Transmembrane_domain			
FT	Domain	575. .593		
FT	/label= Transmembrane_domain			
FT	Domain	617. .635		
FT	/label= Transmembrane_domain			
FT	Region	667. .681		
FT	/label= Poor_loop_region			
FT	Domain	693. .720		
FT	/label= Transmembrane_domain			
XX				
XX				
PN	W0200134805-A2.			
PD				
XX	17-MAY-2001.			
XX				
PF	10-NOV-2000; 2000MO-US031077.			
PR				
XX	12-NOV-1999; 99US-00438997.			
XX	(ABBO) ABBOTT LAB.			
PA				
PI	Masters JN, Vos MH;			
XX				
XX	WPI; 2001-335930/35.			
DR	N-PSDB; AAD05107.			
XX				
PT	Novel human vanilloid receptor gene and encoded polypeptides for			
PT	identifying compounds that modulate vanilloid receptors in human tissues			
PT	and for treating inflammation, arthritis, psoriasis and wound healing.			
XX				
PS	Claim 18; Fig 8; 91pp; English.			
CC	The present sequence is human vanilloid receptor 3 (hVR3) protein.			
CC	Vanilloid receptor protein and its DNA are useful for identifying			
CC	compounds which modulate vanilloid receptors in human tissues, which are			
CC	useful for treating various disease states, including neuropathic pain,			
CC	inflammation, arthritis, rhinitis, pruritus, bladder dysfunction, cluster			
CC	headache, wound healing and psoriasis. Vanilloid receptor DNA is useful			
CC	as standard or reagent in diagnostic immunoassays, as targets for			
CC	pharmaceutical screening assays and also in gene therapy. Vanilloid			
CC	receptor protein is useful for detecting the presence of anti-vanilloid			
CC	receptor derived polypeptide in test samples. Vanilloid receptor			
CC	antibodies are useful for detecting vanilloid receptor polypeptides, for			
CC	screening for diseases or conditions associated with abnormal vanilloid			
CC	receptor production, treating disorders involving capsaicin-sensitive ion			
CC	channels and as diagnostic markers			
XX				
SQ	Sequence 871 AA;			
1	MADSEGGRAAPGAEVAILPGDESGTGGGEAPPLSLIANLFGEGOSGLSPSPADSRPAGP			
Db	1 MADSEGGRAAPGAEVAILPGDESGTGGGEAPPLSLIANLFGEGOSGLSPSPADSRPAGP			
60	60			
61	GDGRPNLPMKQGAERKGVNPIDILBESTLYESSVVPQPKAPMDSLFYGYTHRHSSDN			
Db	61 GDGRPNLPMKQGAERKGVNPIDILBESTLYESSVVPQPKAPMDSLFYGYTHRHSSDN			
120	120			
121	KRMKKTIETKQPOPKAPAPQPPILKVENPILFDIVSRGSTADLDGLPFLTHKKRL			
Db	121 KRMKKTIETKQPOPKAPAPQPPILKVENPILFDIVSRGSTADLDGLPFLTHKKRL			
180	180			
121	KRMKKTIETKQPOPKAPAPQPPILKVENPILFDIVSRGSTADLDGLPFLTHKKRL			
Db	121 KRMKKTIETKQPOPKAPAPQPPILKVENPILFDIVSRGSTADLDGLPFLTHKKRL			
180	180			

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QY 181 TDEEREPSTGKTCI.PKALINLSNGRNDTIPVLDDIAERTGNMREFINSPFDDIYYRGQT 240
DB 181 TDEEREPSTGKTCI.PKALINLSNGRNDTIPVLDDIAERTGNMREFINSPFDDIYYRGQT 240
QY 241 ALHIAIERCKKHYVELLVAGADVAHAQARGFPOKDEGGYFYFGELPLSLAACTNQHPI 300
DB 241 ALHIAIERCKKHYVELLVAGADVAHAQARGFPOKDEGGYFYFGELPLSLAACTNQHPI 300
QY 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLEPDS 360
DB 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLEPDS 360
QY 361 NIEAVLNNDGLSPMLMAAKTKGIGIPOHIIIRREVTDDETRHLSRKFKDMAAGPYVSSLYD 420
DB 361 NIEAVLNNDGLSPMLMAAKTKGIGIPOHIIIRREVTDDETRHLSRKFKDMAAGPYVSSLYD 420
QY 421 LSSLDTCGERASVLEILVYNSKIENRHEMLAVEPINELDRDKMRKGAVSFYINVSYLEC 480
DB 421 LSSLDTCGERASVLEILVYNSKIENRHEMLAVEPINELDRDKMRKGAVSFYINVSYLEC 480
QY 481 AMVIFTLTAAYQPLEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540
DB 481 AMVIFTLTAAYQPLEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540
QY 541 NSLFDGSPQLLYFYISVLYVSAAVLAGIEAVLAVMVFALVGMNNAIYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFYISVLYVSAAVLAGIEAVLAVMVFALVGMNNAIYFTRGLKLTG 600
QY 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
DB 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
QY 661 R0SETSTFLDLFKLTIGMGDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720
DB 661 R0SETSTFLDLFKLTIGMGDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGVSKESKHIWKLQ 736
DB 721 TVGVSKESKHIWKLQ 736

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RESULT 4
AAG65787
ID AAG65787 standard; protein: 871 AA.
XX AAG65787;
XX 30-JAN-2002 (first entry)
XX Human ion channel VR-5 protein sequence.
XX Ion channel; vanilloid receptor; VR-3; VR-5; nootropic; neuroprotective;
XX antiparkinsonian; analgesic; antidiabetic; antiproliferative; cytostatic;
XX antineumatic; antiarthritic; gene therapy; antitense therapy.
XX Homo sapiens.
XX NO200168857-A2.
XX 20-SEP-2001.
XX 15-MAR-2001; 2001WO-US008329.
XX 15-MAR-2000; 2000US-00525420.
XX (MILL-) MILLENNIUM PHARM INC.
XX PA
XX PI
XX Curtis RAD, Cook WJ;
XX WPI: 2001-596911/67.
XX N-PSDB; AA166972; AA166973.
XX Nucleic acid encoding human ion channels referred to as Vanilloid

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PT receptor 3 (VR-3) and VR-5, useful for screening modulators of VR-3 or VR
PT -5 and for treating calcium homeostasis related disorders (e.g. dementia)
PT and pain disorders.
XX
XX Claim 13; Fig 2A-C; 167pp; English.
XX
XX The invention provides nucleic acid encoding human ion channels referred
XX to as Vanilloid receptor 3 (VR-3) and VR-5. The VR-3 or VR-5 proteins can
XX be used to screen for naturally occurring VR-3 or VR-5 ligands or for
XX drugs or compound which modulate VR-3 or VR-5 activity. The VR-3 or VR-5
XX proteins and their modulators (e.g. antitense nucleic acids and anti-VR
XX antibodies) are useful for treating disorders characterized by
XX insufficient or excessive production of VR-3 or VR-5. These disorders are
XX calcium homeostasis related disorders (Alzheimer's disease, dementia,
XX Parkinson's disease), pain disorders (diabetic neuropathy, rheumatoid
XX arthritis) and/or cellular growth and/or proliferation disorders (e.g.
XX cancer). Numerous other examples of these disorders are given in the
XX specification. The present sequence represents the human VR-5
XX
XX Sequence 871 AA:
SQ
Query Match 99.2%; Score 3829; DB 4; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 MADSSGPAPAGGEVAVELFGDSEGTGGEAFPLSTIANFEDEGDSLSPSPADAPAPG 60
1 MADSSGPAPAGGEVAVELFGDSEGTGGEAFPLSTIANFEDEGDSLSPSPADAPAPG 60
61 G0GRPMLRMKFOGAFKGYVNPIDLESTLYESSVVPGRKAPMDSLPYGYTRHSSDN 120
61 G0GRPMLRMKFOGAFKGYVNPIDLESTLYESSVVPGRKAPMDSLPYGYTRHSSDN 120
121 KWRKKKILKOPSPAPAPQPPILKVENRPILEPITVSRSADLDGLPILTKKRL 180
121 KWRKKKILKOPSPAPAPQPPILKVENRPILEPITVSRSADLDGLPILTKKRL 180
122 KWRKKKILKOPSPAPAPQPPILKVENRPILEPITVSRSADLDGLPILTKKRL 180
181 TDEEREPSTGKTCI.PKALINLSNGRNDTIPVLDDIAERTGNMREFINSPFDDIYYRGQT 240
181 TDEEREPSTGKTCI.PKALINLSNGRNDTIPVLDDIAERTGNMREFINSPFDDIYYRGQT 240
241 ALHIAIERCKKHYVELLVAGADVAHAQARGFPOKDEGGYFYFGELPLSLAACTNQHPI 300
241 ALHIAIERCKKHYVELLVAGADVAHAQARGFPOKDEGGYFYFGELPLSLAACTNQHPI 300
301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLEPDS 360
301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLEPDS 360
361 NIEAVLNNDGLSPMLMAAKTKGIGIPOHIIIRREVTDDETRHLSRKFKDMAAGPYVSSLYD 420
361 NIEAVLNNDGLSPMLMAAKTKGIGIPOHIIIRREVTDDETRHLSRKFKDMAAGPYVSSLYD 420
421 LSSLDTCGERASVLEILVYNSKIENRHEMLAVEPINELDRDKMRKGAVSFYINVSYLEC 480
421 LSSLDTCGERASVLEILVYNSKIENRHEMLAVEPINELDRDKMRKGAVSFYINVSYLEC 480
481 AMVIFTLTAAYQPLEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540
481 AMVIFTLTAAYQPLEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540
541 NSLFDGSPQLLYFYISVLYVSAAVLAGIEAVLAVMVFALVGMNNAIYFTRGLKLTG 600
541 NSLFDGSPQLLYFYISVLYVSAAVLAGIEAVLAVMVFALVGMNNAIYFTRGLKLTG 600
601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
661 R0SETSTFLDLFKLTIGMGDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720
661 R0SETSTFLDLFKLTIGMGDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720

QY 721 TVGVSKSKHIMKIQ 736
DB 721 TVGVSKSKHIMKIQ 736

RESULT 5
AAU74935
ID AAU74935 standard; protein; 871 AA.

AC AAU74935;
DT 23-APR-2002 (first entry)

DE Amino acid sequence of human vanilloid receptor-like protein 2a (VR1-2a).

XX Human; vanilloid receptor-like protein 2a; VR1-2a; hypertension;
XX ion-channel protein; pain; osteoarthritis; diabetic neuropathy;
XX neuralgia; nerve injury; neurodegeneration; stroke; inflammation; asthma;
XX allergy; urogenital disorder; incontinence; hypotension;
XX perivascular disease; VR1-related disease; receptor.

OS Homo sapiens.

PN EP1160254-A1.

PD 05-DEC-2001.

PF 25-MAY-2001; 2001EP-00304663.

PR 31-MAY-2000; 2000US-0208156P.

PA (PFI2) PFIZER INC.

PI Shinjo K, Yabuuchi H;

DR WPI: 2002-084359/12.

DR N-PSDB; ABK14002.

PT New human vanilloid receptor-like proteins, useful for identifying

PS Claim 1; Page 17-18; 32pp; English.

XX The present invention relates to a new polypeptide that has a sequence
CC 871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their
CC variants, as defined in the specification. The polypeptide of the
CC invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)
CC or 1900 base pairs (ABK14003) long, or their variants, also defined in
CC the specification. The polypeptides of the invention, which are human
CC vanilloid receptor-like (VR1) proteins, are used to identify specific
CC modulators that are potentially useful for treating pain (of any origin),
CC osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,
CC neurodegeneration, stroke, inflammation, asthma, allergy, urogenital
CC disorders, incontinence, hypo- or hyper-tension and perivascular disease.
CC The molecules of the invention can also be used to raise specific
CC antibodies. The nucleic acid that encodes the polypeptide of the
CC invention is useful for recombinant production of the protein and for
CC preparing transgenic animal models. The polypeptide, antibody and nucleic
CC acid of the invention are also useful as diagnostic agents for
CC determining (susceptibility to) VR1-related diseases. The present amino
CC acid sequence represents the human vanilloid receptor-like protein 2a
CC (VR1-2a) of the invention
SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 5; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSRGPRAGGEVAVELPGDESGTPGCGAFLPLSLANLFEGBDGLSPSPADASRPAGP 60
DB 1 MADSSRGPRAGGEVAVELPGDESGTPGCGAFLPLSLANLFEGBDGLSPSPADASRPAGP 60

QY 61 GDSRPULRMKFGQAFRRKGVNPIIDLESTLYESSVVPGRKAMDSLFDYGYRRHSSDN 120
DB 61 GDSRPULRMKFGQAFRRKGVNPIIDLESTLYESSVVPGRKAMDSLFDYGYRRHSSDN 120
QY 121 KWRKKKIIKKOPSPAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLLPILTHKKRL 180
DB 121 KWRKKKIIKKOPSPAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLLPILTHKKRL 180
QY 181 TDEFRPEPTGKTCLEKALLNLSNGRNDTIPVLDDIAERTGNMREPFINSFRRDIYYRGOT 240
DB 181 TDEFRPEPTGKTCLEKALLNLSNGRNDTIPVLDDIAERTGNMREPFINSFRRDIYYRGOT 240
QY 241 ALHIAIERCKHVELVLAQADVHAQARGFRFQPDQEGYFFYFGEPLSLAQTQPHI 300
DB 241 ALHIAIERCKHVELVLAQADVHAQARGFRFQPDQEGYFFYFGEPLSLAQTQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKYTKMYDLILKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKYTKMYDLILKCARLFPDS 360
QY 361 NLEAVLNNDGLSPIMAAATGKIGIHOHTIRREVTDEDRHLRKRKDMAYGVYSLYD 420
DB 361 NLEAVLNNDGLSPIMAAATGKIGIHOHTIRREVTDEDRHLRKRKDMAYGVYSLYD 420
QY 421 LSLDTCGEASVLEILVYNSKIENHMLAVEPINELDKMRKGAVSFYINVSYL 480
DB 421 LSLDTCGEASVLEILVYNSKIENHMLAVEPINELDKMRKGAVSFYINVSYL 480
QY 481 AMVIFTLTAYYQPLESTPEPYRTTYDYLRLAGEVITLTGVLFFFTNIDKLFMKKCPGV 540
DB 481 AMVIFTLTAYYQPLESTPEPYRTTYDYLRLAGEVITLTGVLFFFTNIDKLFMKKCPGV 540
QY 541 NSLFDIDSGFQLLYFIYSVAVISAALYLAGIEAYLAVMFPAVLGMNNALYFRGKLTG 600
DB 541 NSLFDIDSGFQLLYFIYSVAVISAALYLAGIEAYLAVMFPAVLGMNNALYFRGKLTG 600
QY 601 TYSIMIOKILFNDLFRFLVYLLFMIGVASALVSLNPCANNKVCNEDQNTCTVTPYSPC 660
DB 601 TYSIMIOKILFNDLFRFLVYLLFMIGVASALVSLNPCANNKVCNEDQNTCTVTPYSPC 660
QY 661 RDSFTFTFLDLFLKLTIGMDLMLSTKYVVFVFIILVYIILTFVILLNMLIALMGE 720
DB 661 RDSFTFTFLDLFLKLTIGMDLMLSTKYVVFVFIILVYIILTFVILLNMLIALMGE 720
QY 721 TVGVSKSKHIMKIQ 736
DB 721 TVGVSKSKHIMKIQ 736

RESULT 6
ABB79191
ID ABB79191 standard; protein; 871 AA.

AC ABB79191;

DT 07-AUG-2002 (first entry)

DE Human VR4 protein SEQ ID NO:2.

XX Human; VR4; vanilloid 4 receptor; receptor; osteopathic; anti-rheumatic;
XX antiautarchic; vulnery; analgesic; gene therapy; cartilage; bone;
XX larynx; auditory canal; intravertebral disc; ligament; tendon;
XX joint capsule; bone development disorder; osteoporosis; osteoarthritis;
XX joint destruction; rheumatoid arthritis.

OS Homo sapiens.

PN WO200234280-A2.

PD 02-MAY-2002.

PF 25-OCT-2001; 2001WO-GB004739.

PR 25-OCT-2000; 2000GB-00026114.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA Davis JB, Gunthorpe MJ, Egerton J, Smart D;
 PI WPI: 2002-471426/50.
 XX N-PSDB; ABN67645.
 DR
 XX
 XX Use of vanilloid 4 receptor polypeptide/polynucleotide, a modulator of
 PT the polypeptide or an antisense polynucleotide for the polynucleotide, for
 PT manufacture of a medicament for treating cartilage and/or bone diseases.
 XX
 XX Claim 8; Page 22; 30pp; English.
 XX
 CC The present sequence represents human vanilloid 4 receptor (VR4). VR4 has
 CC osteopathic, antineumatic, antiarthritic, vulnary and analgesic
 CC activities. VR4 proteins and polynucleotide sequences can be used in
 CC modulating VR4 activity, in gene therapy and in antisense gene therapy.
 CC VR4 is useful for the manufacture of a medicament for treating diseases
 CC of cartilage and/or bone, or for the treatment of pain associated with
 CC it, where the disease is one affecting the larynx, auditory canal,
 CC intervertebral discs, ligaments, tendons and joint capsules, or a disease
 CC associated with bone development including osteoporosis, or diseases
 CC involving joint destruction such as rheumatoid arthritis or
 CC osteoarthritis, and the pain is associated with rheumatoid arthritis or
 CC osteoarthritis
 CC
 SQ Sequence 871 AA;
 Query Match 99.2%; Score 3829; DB 5; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAASSSEPRAGPRGVALLPDESGTPGGEAFPLSLANLFEGRGSLSPSPADSRPAGP 60
 DB 1 MAOSSSEPRAGPRGVALLPDESGTPGGEAFPLSLANLFEGRGSLSPSPADSRPAGP 60
 QY 61 GDGPNRMKFGQAFKGVNPIDLESTLYESSVVGPKKAPMDSLFDTYVHHSSDN 120
 DB 61 GDGPNRMKFGQAFKGVNPIDLESTLYESSVVGPKKAPMDSLFDTYVHHSSDN 120
 QY 121 KRWKRTIIEKQPSKAPAPPPILKVNRPILFDIVSRGSLADLDGLPFLTHKKRL 180
 DB 121 KRWKRTIIEKQPSKAPAPPPILKVNRPILFDIVSRGSLADLDGLPFLTHKKRL 180
 QY 181 TDEFFRPSSTGKTLKPLALNLSNGRNDTTPVLDIARCGMGEFINSPPRDITYRGQT 240
 DB 181 TDEFFRPSSTGKTLKPLALNLSNGRNDTTPVLDIARCGMGEFINSPPRDITYRGQT 240
 QY 241 ALHAIARRCHGYVELVAQAGADVAQAARGFPOKDEGFFYFGEPLSLAICTNPHI 300
 DB 241 ALHAIARRCHGYVELVAQAGADVAQAARGFPOKDEGFFYFGEPLSLAICTNPHI 300
 QY 301 VNYLTENPHKADMRKODSRGNTVLAHVAIADNTRENTKFTVTMTDLILKCARLPDS 360
 DB 301 VNYLTENPHKADMRKODSRGNTVLAHVAIADNTRENTKFTVTMTDLILKCARLPDS 360
 QY 361 NLEAVANNDSPLMMAKTKGTIGFOHITREVTDETRLSKRFKDMAGPYSSLYD 420
 DB 361 NLEAVANNDSPLMMAKTKGTIGFOHITREVTDETRLSKRFKDMAGPYSSLYD 420
 QY 421 LLSLDTGCEASVLEIIVNSKIEHRHMLAVEPINEILRDKMRKFGAVSYFINVSYLC 480
 DB 421 LLSLDTGCEASVLEIIVNSKIEHRHMLAVEPINEILRDKMRKFGAVSYFINVSYLC 480
 QY 481 AMVIFLTAYVQPLEGTPPYRYRTVDYLRLAGEVITLFTGVLPFTNFKLPMKCCPGV 540
 DB 481 AMVIFLTAYVQPLEGTPPYRYRTVDYLRLAGEVITLFTGVLPFTNFKLPMKCCPGV 540
 QY 541 NSLFIIDSGFOLLVPIYSVLVVSALVYAGTEAVYANVWVPLVGMNVALFTGKLKLG 600
 DB 541 NSLFIIDSGFOLLVPIYSVLVVSALVYAGTEAVYANVWVPLVGMNVALFTGKLKLG 600

QY 601 TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNCPANKVCNEDQNTCTVPTPSC 660
 DB 601 TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNCPANKVCNEDQNTCTVPTPSC 660
 QY 661 RDSSTSTFLDLFKTLTGMDLEMLSTKYPVFTLLVATYITLFFVLLNMLLMGE 720
 DB 661 RDSSTSTFLDLFKTLTGMDLEMLSTKYPVFTLLVATYITLFFVLLNMLLMGE 720
 QY 721 TWGVSKESKHIMKQLQ 736
 DB 721 TWGVSKESKHIMKQLQ 736
 RESULT 7
 ADG64947
 ID ADG64947 standard; protein; 871 AA.
 AC ADG64947;
 XX 11-MAR-2004 (first entry)
 DT VANILREP4 polypeptide of the invention.
 XX
 DE VANILREP4 polypeptide of the invention.
 XX
 XX vanilrep4; VR4; Analgesic; cerebroprotective; antiinflammatory;
 KW antidiabetic; anorectic; vasotropic; utropachic; ischemia;
 KW neurodegeneration; inflammatory disorder; irritable bowel syndrome;
 KW diabetes; obesity.
 KW
 XX Homo sapiens.
 OS
 XX EPI170365-A1.
 XX 09-JAN-2002.
 PD 04-JUL-2000; 2000EP-00202352.
 PF 04-JUL-2000; 2000EP-00202352.
 PR 04-JUL-2000; 2000EP-00202352.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA Smith G, Hayes PD, Smart D, Davis JB, Kelsell RE;
 PI WPI: 2002-156636/21.
 DR N-PSDB; ADG64946.
 XX
 XX Polypeptide of ion channel family polypeptides, designated vanilrep4,
 PT useful as a vaccine for inducing immune response against diseases such as
 PT neuropathies, algesia, nerve injury, ischemia, stroke, incontinence,
 PT diabetes, obesity.
 PT
 PS Claim 1; SEQ ID NO 2; 29pp; English.
 XX
 CC The present invention relates to a polypeptide of ion channel family
 CC polypeptides, vanilrep4 (VR4). The peptides are useful for treating pain
 CC (e.g. chronic pain, neuropathic pain, post-operative pain, rheumatoid
 CC arthritic pain), neuralgia, neuropathies, algesia, nerve injury,
 CC ischemia, neurodegeneration, stroke, incontinence, inflammatory
 CC disorders, irritable bowel syndrome, diabetes or obesity. Fragments of
 CC the protein are useful for producing full-length polypeptides by peptide
 CC synthesis therefore the variants may also be employed as intermediate for
 CC producing full-length polypeptide. The proteins are also useful for
 CC identifying agonists or antagonists of peptide activity and expression.
 CC The peptide is useful as diagnostic reagents for diagnosing a disease or
 CC a susceptibility to a disease by detecting mutations in the associated
 CC gene, and is also useful for chromosome localization studies and tissue
 CC expression studies. The peptide is useful for producing transgenic
 CC animals, which include knock-in animals (in which an animal gene is
 CC replaced by human equivalent within the genome of the animal), useful in
 CC drug discovery process, for target validation, where the compound is
 CC specific for human target. Peptides and Ab is useful for confounding
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA in cells. The peptides are useful as vaccines for

CC inducing an immunological response in a mammal. The present sequence
 CC represents VANILRP4 polypeptide.

XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 5; Length 871;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
QY 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
DB 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
QY 121 KMRKKKIIKOPQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRL 180
DB 121 KMRKKKIIKOPQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRL 180
QY 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLLDIAERTGNMREFINSFPDIYYRGOT 240
DB 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLLDIAERTGNMREFINSFPDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVAHQARGRFFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
DB 241 ALHIAIERCKHYVELLVAQADVAHQARGRFFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
QY 301 VNYLTENPHKKAAMRQDSRGNTVLAHVAIADNTRENTKFTYKMDLLKCARLPDPS 360
DB 301 VNYLTENPHKKAAMRQDSRGNTVLAHVAIADNTRENTKFTYKMDLLKCARLPDPS 360
QY 361 NLEAVLNDGSLPIMAAKTGKIGIFQHIIRREVTDEDPRLSRKCKDWAYGVSLSYD 420
DB 361 NLEAVLNDGSLPIMAAKTGKIGIFQHIIRREVTDEDPRLSRKCKDWAYGVSLSYD 420
QY 421 LSSLDTCGEBASYLELIVNSKIENHEMLAVEPINELLRDKWRKFGAVSFYINVSYL 480
DB 421 LSSLDTCGEBASYLELIVNSKIENHEMLAVEPINELLRDKWRKFGAVSFYINVSYL 480
QY 481 ANVIFLTAAYOPLBETPPPYRTTYDYLRAGEVITLTGTGVLFFFTNTKDLPMKCCPV 540
DB 481 ANVIFLTAAYOPLBETPPPYRTTYDYLRAGEVITLTGTGVLFFFTNTKDLPMKCCPV 540
QY 541 NSLFLDGSFQLYFIYSVLIVSAALYLAGIEAYLAVMFAYLGMNNAALYFTRGLKLG 600
DB 541 NSLFLDGSFQLYFIYSVLIVSAALYLAGIEAYLAVMFAYLGMNNAALYFTRGLKLG 600
QY 601 TYSIMQKILFKDLFFLLVYLLFMTGYASALVSLINPCANMKVCNEDQNCCTVPTPSC 660
DB 601 TYSIMQKILFKDLFFLLVYLLFMTGYASALVSLINPCANMKVCNEDQNCCTVPTPSC 660
QY 661 RDSFESTFLDLDFKLTIGMDLEMLSKRYPVVFITLVYIILTFVLLNMLTALMGE 720
DB 661 RDSFESTFLDLDFKLTIGMDLEMLSKRYPVVFITLVYIILTFVLLNMLTALMGE 720
QY 721 TVGQVSKESKHIWKLQ 736
DB 721 TVGQVSKESKHIWKLQ 736

```

RESULT 8

ADG32562

ADG32562 standard; protein; 871 AA.

AC ADG32562;

XX 26-FEB-2004 (first entry)

DE Human TRPV4 protein, member of the vanilloid receptor family.

XX human; vanilloid receptor; VR; pain perception; TRPV3; VR1S; VR1X; VR4;

KM TRPV7, TRPV4; VR13; OTRPC4; TRPM8; TRPV; trkA; inflammation;
 KM skin disorder; cancer; analgesic; antiinflammatory; dermatological;
 KM cytostatic.

OS Homo sapiens.

XX WO2002101045-A2.

XX 19-DEC-2002.

PD 13-JUN-2002; 2002WO-EP065520.

XX 13-JUN-2001; 2001US-0297835P.

PR 22-JAN-2002; 2002US-0351238P.

PR 29-JAN-2002; 2002US-0352914P.

PR 12-FEB-2002; 2002US-0357161P.

PR 15-MAY-2002; 2002US-0381086P.

PR 16-MAY-2002; 2002US-0381739P.

XX (NOV) NOVARTIS AG.

PA (IRMT-) IRM LLC.

PI Patapoutian A, Song C, Ganju P, Peier A, McIntyre P, Bevan S;

XX WPI; 2003-156962/15.

DR N-PDB; ADG32561.

XX New isolated TRPV3, TRPV4 or TRPM8 vanilloid receptor nucleic acid

PT molecule and polypeptides, useful for the diagnosis and treatment of

PT disorders such as pain, inflammation, skin diseases and cancer.

PS Claim 69; SEQ ID NO 17; 197pp; English.

XX This invention relates to novel vanilloid receptor (VR) related nucleic

CC acids and encoded proteins thereof. Specifically, it refers to certain

CC members of the VR family that are involved in pain perception, in

CC particular, TRPV3 (previously known as VR1S, VR1X, VR4 & TRPV7), TRPV4

CC (previously known as VR13 & OTRPC4) and TRPM8 (previously known as TRPX).

CC Furthermore, this invention includes trkA pain specific genes expressed

CC in the sensory neurons of the dorsal root ganglia. Accordingly, such

CC compositions can be useful for the diagnosis, treatment and prevention of

CC pain, inflammation, skin disorders and cancer, and so exhibit analgesic,

CC antiinflammatory, dermatological and cytostatic activities. This

CC polypeptide sequence is the human TRPV4 protein of the invention.

XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 7; Length 871;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
QY 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
DB 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
QY 121 KMRKKKIIKOPQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRL 180
DB 121 KMRKKKIIKOPQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRL 180
QY 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLLDIAERTGNMREFINSFPDIYYRGOT 240
DB 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLLDIAERTGNMREFINSFPDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVAHQARGRFFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
DB 241 ALHIAIERCKHYVELLVAQADVAHQARGRFFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
QY 301 VNYLTENPHKKAAMRQDSRGNTVLAHVAIADNTRENTKFTYKMDLLKCARLPDPS 360

```

Db 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTVKMYDLILKCARLFPDS 360
 Qy 361 NLEAVLNNDGLSPMLMAAKTGKIGIPOHIIIRREVTDEDRHLSRKFKDMAVGPVSSLYD 420
 Db 361 NLEAVLNNDGLSPMLMAAKTGKIGIPOHIIIRREVTDEDRHLSRKFKDMAVGPVSSLYD 420
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480
 Qy 481 AMVITLTAYYQPLEGPPYPTTYDYRLAGEVITLFFGVLPFTNIDLEMKKCPGV 540
 Db 481 AMVITLTAYYQPLEGPPYPTTYDYRLAGEVITLFFGVLPFTNIDLEMKKCPGV 540
 Qy 541 NSLFDGSPQLLYFTYSVLYVSAALYLAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600
 Db 541 NSLFDGSPQLLYFTYSVLYVSAALYLAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600
 Qy 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 Db 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLALMGE 720
 Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLALMGE 720
 Qy 721 TVGQVSKSKHIMKLQ 736
 Db 721 TVGQVSKSKHIMKLQ 736

RESULT 9
 ADL71047
 ID ADL71047 standard; protein; 871 AA.
 AC ADL71047;
 DT 20-MAY-2004 (first entry)
 XX
 DE Type II collagen expression promoting protein, seq id 40.
 XX
 KM Osteopathic; antiinflammatory; antirheumatic; antiarthritic;
 KM gene therapy; type II collagen; expression; cartilage disease;
 KM osteoarthritis; cartilage defect; rheumatoid arthritis; human.
 OS Homo sapiens.
 XX
 PN WO2003087375-A1.
 PD 23-OCT-2003.
 XX
 PF 16-APR-2003; 2003WO-JP004802.
 XX
 PR 16-APR-2002; 2002JP-00113908.
 PR 19-APR-2002; 2002US-0373594P.
 XX
 PA (ASAH) ASAH KASEI KK.
 XX
 PI Matsuda A, Honda G, Muramatsu S;
 XX
 DR WPI; 2003-845331/78.
 DR N-PSDB; ADL71046.
 XX
 PT New purified protein that promotes type II collagen expression, useful
 PT for preventing and treating a cartilage disease, e.g. osteoarthritis,
 PT cartilage defect, or rheumatoid arthritis.
 XX
 PS Claim 1; SEQ ID NO 40; 271pp; English.
 CC The invention relates to a purified protein (I) that promotes type II
 CC collagen expression. Also disclosed is an isolated polynucleotide
 CC encoding (I), a recombinant vector comprising the polynucleotide and a
 CC gene therapeutic agent comprising the recombinant vector as an active

CC ingredient. The proteins, genes, agents and methods are useful for
 CC preventing and treating a cartilage disease, e.g. osteoarthritis,
 CC cartilage defect, or rheumatoid arthritis. The current sequence
 CC represents a human protein that promotes type II collagen expression.
 XX
 SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 7; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSSGPRAPGEVAVELPDGSGTGGRAPISSLANIPEGDGSLSPSPAPASPA 60
 Db 1 MADSSGPRAPGEVAVELPDGSGTGGRAPISSLANIPEGDGSLSPSPAPASPA 60
 Qy 61 GDRPMLRMKFGAFKGPVNPIDLESTLYESSVVPGRPKAMDSLFDYGYRHSSDN 120
 Db 61 GDRPMLRMKFGAFKGPVNPIDLESTLYESSVVPGRPKAMDSLFDYGYRHSSDN 120
 Qy 121 KRRRKXIEKQPSAPAPAPQPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 180
 Db 121 KRRRKXIEKQPSAPAPAPQPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 180
 Qy 181 TDEEFPSTGKTCLEKALNLSNGRNDIIPVLDIAERTGNRREFINSPPRIYRGOT 240
 Db 181 TDEEFPSTGKTCLEKALNLSNGRNDIIPVLDIAERTGNRREFINSPPRIYRGOT 240
 Qy 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQKDEGGYFYFGEIPLSLAATQPHI 300
 Db 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQKDEGGYFYFGEIPLSLAATQPHI 300
 Qy 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTVKMYDLILKCARLFPDS 360
 Db 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTVKMYDLILKCARLFPDS 360
 Qy 361 NLEAVLNNDGLSPMLMAAKTGKIGIPOHIIIRREVTDEDRHLSRKFKDMAVGPVSSLYD 420
 Db 361 NLEAVLNNDGLSPMLMAAKTGKIGIPOHIIIRREVTDEDRHLSRKFKDMAVGPVSSLYD 420
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480
 Qy 481 AMVITLTAYYQPLEGPPYPTTYDYRLAGEVITLFFGVLPFTNIDLEMKKCPGV 540
 Db 481 AMVITLTAYYQPLEGPPYPTTYDYRLAGEVITLFFGVLPFTNIDLEMKKCPGV 540
 Qy 541 NSLFDGSPQLLYFTYSVLYVSAALYLAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600
 Db 541 NSLFDGSPQLLYFTYSVLYVSAALYLAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600
 Qy 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 Db 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLALMGE 720
 Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLALMGE 720
 Qy 721 TVGQVSKSKHIMKLQ 736
 Db 721 TVGQVSKSKHIMKLQ 736

RESULT 10
 ADI81584
 ID ADI81584 standard; protein; 871 AA.
 AC ADI81584;
 DT 22-APR-2004 (first entry)
 XX
 DE Human vanilloid receptor-related channel like protein.

XX Human; calcium entry modulator; CD4536; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KM Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 XX hepatitis; cirrhosis; kidney disease; glomerulonephritis.
 OS Homo sapiens.
 PN US2004009537-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 13-JAN-2003; 2003US-00342844.
 XX
 PR 11-JAN-2002; 2002US-0347459P.
 XX 02-AUG-2002; 2002US-0401171P.
 PR 20-AUG-2002; 2002US-0405678P.
 XX
 PA (ROOS/) ROOS J.
 PA (STAU/) STAUDERMAN K.
 PA (VELI/) VELICELEBI G.
 XX
 PI Roos J, Stauderman K, Velicelebi G;
 XX
 DR WPI; 2004-090465/09.
 DR N-PSDB; ADI81583.
 XX
 PT Identifying an agent that modulates intracellular calcium levels, useful
 PT for treating diseases associated with calcium dysregulation (e.g.
 PT cancer), comprises monitoring the effects of the agent on store-operated
 PT calcium entry.
 XX
 PS Disclosure; SEQ ID NO 54; 55pp; English.
 XX
 CC The invention relates to identifying an agent that modulates
 CC intracellular calcium comprising monitoring the effects of the agent on
 CC store-operated calcium entry comprising contacting one or more test cells
 CC or their portion comprising one or more proteins that is (are) at least
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or
 CC CG5842 over at least about 40% of the encoded protein (and that provides
 CC for store-operated calcium entry with a test agent), where the portion of
 CC the cell comprises the proteins, monitoring the effect(s) of the test
 CC compound on store-operated calcium entry and identifying a test agent as
 CC an agent if it has an effect on store-operated calcium entry. Also
 CC included are a method of modulating store-operated calcium entry
 CC (comprising modulating the level of expression of, activity of or
 CC molecular interactions of a protein in a cell that has altered store-
 CC operated calcium entry, where the protein is at least about 35%
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842
 CC over at least about 40% of the encoded protein and that provides for
 CC store-operated calcium entry, and where store-operated calcium transport
 CC into the cell is modulated, and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC ADI81644 and ADI81645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 XX
 SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 8; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MADSSGPRAGPGEVAVELPDDESGTGGGEAFPLSSLANLFEGBDGSISPADASRPAGP 60

|||||
 Db 1 MADSSGPRAGPGEVAVELPDDESGTGGGEAFPLSSLANLFEGBDGSISPADASRPAGP 60
 Qy GDERPVLRMKFOGAFKGVNPTDLESTLYESSVPGPKKAWMDSIFDGTGRHSSDN 120
 Db 61 GDERPVLRMKFOGAFKGVNPTDLESTLYESSVPGPKKAWMDSIFDGTGRHSSDN 120
 Qy KRWKRTIIEKOPSPAPAPQPPILKVFRRPILFDIVSGSTADLDGLPFLTHKRL 180
 Db 121 KRWKRTIIEKOPSPAPAPQPPILKVFRRPILFDIVSGSTADLDGLPFLTHKRL 180
 Qy 121 KRWKRTIIEKOPSPAPAPQPPILKVFRRPILFDIVSGSTADLDGLPFLTHKRL 180
 Db 121 KRWKRTIIEKOPSPAPAPQPPILKVFRRPILFDIVSGSTADLDGLPFLTHKRL 180
 Qy 181 TDEEPREPSTGKCTLPKALNLSNGRNDTIPVLLDIAERTGNREFINSFPRDIYRGQT 240
 Db 181 TDEEPREPSTGKCTLPKALNLSNGRNDTIPVLLDIAERTGNREFINSFPRDIYRGQT 240
 Qy 241 ALHIALERCKHVELLVAGADVAHQARREFQPPDEGGYFYFGLPLSLAQTQPHI 300
 Db 241 ALHIALERCKHVELLVAGADVAHQARREFQPPDEGGYFYFGLPLSLAQTQPHI 300
 Qy 301 VNYLTENPHKKADMRRODSRGNTVLAALVAIAENTRENTKFTKMDLLKCARLPDS 360
 Db 301 VNYLTENPHKKADMRRODSRGNTVLAALVAIAENTRENTKFTKMDLLKCARLPDS 360
 Qy 361 NLEAVINNDGLSPDMAAKTKIGIFQHIIRREVTDETRHLSRKKDMAVGPVSSLYD 420
 Db 361 NLEAVINNDGLSPDMAAKTKIGIFQHIIRREVTDETRHLSRKKDMAVGPVSSLYD 420
 Qy 421 LSSLDCGGEASVLELVNSKLENHEMLAVSPINELLRDKRKGAVSFYNNVYL 480
 Db 421 LSSLDCGGEASVLELVNSKLENHEMLAVSPINELLRDKRKGAVSFYNNVYL 480
 Qy 481 AMVIFLTIAVYOPLEGTPPYPTVTDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGV 540
 Db 481 AMVIFLTIAVYOPLEGTPPYPTVTDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGV 540
 Qy 541 NSIFIDSGQLVFTIVSALYLAGIEAYLAWVPALVGMNNAVFTRGKLTG 600
 Db 541 NSIFIDSGQLVFTIVSALYLAGIEAYLAWVPALVGMNNAVFTRGKLTG 600
 Qy 601 TVSIMOKLIFKDLFFLLVYLLFMIGVASVLSLPCANMVCNEDQNCVPTPSC 660
 Db 601 TVSIMOKLIFKDLFFLLVYLLFMIGVASVLSLPCANMVCNEDQNCVPTPSC 660
 Qy 661 RDEETSTFLDLFKLTIGMDLEMLSTKYPVFTLLVYLLFVLLNMLIALMGE 720
 Db 661 RDEETSTFLDLFKLTIGMDLEMLSTKYPVFTLLVYLLFVLLNMLIALMGE 720
 Qy 721 TVGVSKESKHIMKIQ 736
 Db 721 TVGVSKESKHIMKIQ 736
 RESULT 11
 ADI81608
 ID ADI81608 standard; protein; 871 AA.
 XX
 AC ADI81608;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human OTRPC4 cation channel.
 XX
 XX Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KM Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.
 XX
 OS Homo sapiens.
 XX
 PN US2004009537-A1.
 PD 15-JAN-2004.
 XX

PF 13-JAN-2003; 2003US-00342844.
 XX
 PR 11-JAN-2002; 2002US-0347459P.
 PR 02-AUG-2002; 2002US-0401171P.
 PR 20-AUG-2002; 2002US-0405678P.
 XX
 PA (ROOS/) ROOS J.
 PA (STAU/) STAUDERMAN K.
 PA (VELI/) VELICELEBI G.
 PI Roos J, Stauderman K, Velicelebi G;
 XX
 DR WPI; 2004-090465/09.
 DR N-PSDB; AD181607.
 XX
 PT Identifying an agent that modulates intracellular calcium levels, useful
 PT for treating diseases associated with calcium dysregulation (e.g.
 PT cancer), comprises monitoring the effects of the agent on store-operated
 PT calcium entry.
 XX
 PS Disclosure; SEQ ID NO 78; 55pp; English.
 XX
 CC The invention relates to identifying an agent that modulates
 CC intracellular calcium comprises monitoring the effects of the agent on
 CC store-operated calcium entry comprising contacting one or more test cells
 CC or their portion comprising one or more proteins that is (are) at least
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or
 CC CG5842 over at least about 40% of the encoded protein (and that provides
 CC for store-operated calcium entry with a test agent), where the portion of
 CC the cell comprises the proteins, monitoring the effect(s) of the test
 CC compound on store-operated calcium entry and identifying a test agent as
 CC an agent if it has an effect on store-operated calcium entry. Also
 CC included are a method of modulating store-operated calcium entry
 CC (comprising modulating the level of, expression of, activity of or
 CC molecular interactions of a protein in a cell that has altered store-
 CC operated calcium entry, where the protein is at least about 35%
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842
 CC over at least about 40% of the encoded protein and that provides for
 CC store-operated calcium entry, and where store-operated calcium transport
 CC into the cell is modulated) and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC AD181644 and AD181645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 XX
 SQ Sequence 871 AA;
 Query Match 99.2%; Score 3829; DB 8; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 TDEEFREPSTGKTCIPKALNLSNGRNDTIPVLLDIAERTGNMREIFNSPFDIYYRGQT 240
 QY ALHAIERRCKHYVELLVAQADVHAQARGFPQKQGGYFYGELPLSLAATNCPHI 300
 DB 241 ALHAIERRCKHYVELLVAQADVHAQARGFPQKQGGYFYGELPLSLAATNCPHI 300
 QY VNYLTENPHKKADMRRODSRGNTVLAHVAIADNTRENTKFTVMYDILLKCARLPDS 360
 DB 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIADNTRENTKFTVMYDILLKCARLPDS 360
 QY NLEAVLNNDGLSPDMAAKTKGIGIFQHIIRREYTDPTDTHLSKFKDMAGPYSSLYD 420
 DB 361 NLEAVLNNDGLSPDMAAKTKGIGIFQHIIRREYTDPTDTHLSKFKDMAGPYSSLYD 420
 QY LSSLDTCGEASVLEILVYNSKIENREHMLAVEPINELBDKMKFGAVSFYINVSYL 480
 DB 421 LSSLDTCGEASVLEILVYNSKIENREHMLAVEPINELBDKMKFGAVSFYINVSYL 480
 QY AMVIFLTAYYQPLGTPPYPRRTVDYLRAGEVITLFTGVLEFFTNIKDLFMKCPGV 540
 DB 481 AMVIFLTAYYQPLGTPPYPRRTVDYLRAGEVITLFTGVLEFFTNIKDLFMKCPGV 540
 QY NSLPIDSSPOLVFTYVSVIVSALYLAGI EAVLAVMVPALVIGMNNALYFTRGLKLTG 600
 DB 541 NSLPIDSSPOLVFTYVSVIVSALYLAGI EAVLAVMVPALVIGMNNALYFTRGLKLTG 600
 QY TYSIMIGKILFKDLFRFLVYLIFMIGYASALVSLNPCAMKVCNEDQNCVPTYPSC 660
 DB 601 TYSIMIGKILFKDLFRFLVYLIFMIGYASALVSLNPCAMKVCNEDQNCVPTYPSC 660
 QY RDSSTPSTFLIDLEKLTIGMDLEMSSTKYPVVFILLVYIILTVLLNMLIALMGE 720
 DB 661 RDSSTPSTFLIDLEKLTIGMDLEMSSTKYPVVFILLVYIILTVLLNMLIALMGE 720
 QY RDSSTPSTFLIDLEKLTIGMDLEMSSTKYPVVFILLVYIILTVLLNMLIALMGE 720
 DB 721 RDSSTPSTFLIDLEKLTIGMDLEMSSTKYPVVFILLVYIILTVLLNMLIALMGE 720
 QY TVGQVSKSKHIMKLQ 736
 DB 721 TVGQVSKSKHIMKLQ 736

RESULT 12
 AD181588
 ID AD181588 standard; protein: 871 AA.
 XX
 AC AD181588;
 XX
 DT 22-Apr-2004 (first entry)
 XX
 DB Human vanilloid receptor-like channel 2.
 XX
 KW Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.
 XX
 OS Homo sapiens.
 XX
 PN US2004009537-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 13-JAN-2003; 2003US-00342844.
 XX
 PR 11-JAN-2002; 2002US-0347459P.
 PR 02-AUG-2002; 2002US-0401171P.
 PR 20-AUG-2002; 2002US-0405678P.
 XX
 PA (ROOS/) ROOS J.
 PA (STAU/) STAUDERMAN K.
 PA (VELI/) VELICELEBI G.
 PI Roos J, Stauderman K, Velicelebi G;
 XX

DR WPI: 2004-090465/09.
 DR N-PSDB; ADI81587.
 PT Identifying an agent that modulates intracellular calcium levels, useful
 PT for treating diseases associated with calcium dysregulation (e.g.
 PT cancer), comprises monitoring the effects of the agent on store-operated
 PT calcium entry.
 XX
 XX Disclosure; SEQ ID NO 58; 55pp; English.
 CC The invention relates to identifying an agent that modulates
 CC intracellular calcium comprises monitoring the effects of the agent on
 CC store-operated calcium entry comprising contacting one or more test cells
 CC or their portion comprising one or more proteins that is (are) at least
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or
 CC CG5842 over at least about 40% of the encoded protein (and that provides
 CC for store-operated calcium entry with a test agent), where the portion of
 CC the cell comprises the proteins, monitoring the effect(s) of the test
 CC compound on store-operated calcium entry and identifying a test agent as
 CC an agent if it has an effect on store-operated calcium entry. Also
 CC included are a method of modulating store-operated calcium entry
 CC (comprising modulating the level of, expression of, activity of or
 CC molecular interactions of a protein in a cell that has altered store-
 CC operated calcium entry, where the protein is at least about 35%
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842
 CC over at least about 40% of the encoded protein and that provides for
 CC store-operated calcium entry, and where store-operated calcium transport
 CC into the cell is modulated) and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC ADI81644 and ADI81645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 CC
 CC Sequence 871 AA:
 SO
 Query Match 99.2%; Score 3829; DB 8; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 361 NLEAVLNNDGLSLMMAAKTGKIGI FQHIIRREVTJEDTHTLSKFKDMAYGPPVSSLYD 420
 QY 421 LSSLDTCGEASVTEILVYNSKIENRHEMLAVEPINELDKMKPKGAVSYINVSYL 480
 DB 421 LSSLDTCGEASVTEILVYNSKIENRHEMLAVEPINELDKMKPKGAVSYINVSYL 480
 QY 481 AMVIFTLTAAYOPLBGPVPYRRTVDYRLAEVITLFTGLVFFFTNIDLPKKKPGV 540
 DB 481 AMVIFTLTAAYOPLBGPVPYRRTVDYRLAEVITLFTGLVFFFTNIDLPKKKPGV 540
 QY 541 NSLFDGSPQLVFIYSVLVYSAALYAGIEAYLAWVPALVGMNNALYFRGLKLTG 600
 DB 541 NSLFDGSPQLVFIYSVLVYSAALYAGIEAYLAWVPALVGMNNALYFRGLKLTG 600
 QY 601 TYSIMTOKILFKDLFFRLVYLLFMIGYASALVSLNPNAMKVCNEDQNTCTVPTPSC 660
 DB 601 TYSIMTOKILFKDLFFRLVYLLFMIGYASALVSLNPNAMKVCNEDQNTCTVPTPSC 660
 QY 661 RDEETSTFLDLEFKLTIGMDLEMLSTKYPVVFITLVYTIIFVLLNMLLMGE 720
 DB 661 RDEETSTFLDLEFKLTIGMDLEMLSTKYPVVFITLVYTIIFVLLNMLLMGE 720
 QY 721 TVGQVSKSKHIMKLTQ 736
 DB 721 TVGQVSKSKHIMKLTQ 736
 RESULT 13
 ABB98197
 ID ABB98197 standard; protein; 871 AA.
 AC ABB98197;
 DT 12-DEC-2002 (first entry)
 XX Human VR-OAC amino acid sequence.
 KW Human: VR-OAC: vanilloid receptor-related osmotically activated channel;
 KW anti-HIV; antistatic; immunomodulator; cerebroprotective;
 KW antidiabetic; antifertility; auditory; antipruritic; dermatological;
 KW antipsychotic; antiallergic; anorectic; neuroprotective;
 KW ophthalmological; nootropic; cytosstatic; nephroretropic; hypotensive;
 KW analgesic; mechanoreception; mechanosensation; hearing disorder; HIV;
 KW Human immunodeficiency virus; obesity; vertigo; motion sickness;
 KW neurological disorder; ataxia; male infertility; immune dysfunction;
 KW diabetes mellitus; chronic obstructive lung disorder; bronchial asthma;
 KW sexual dysfunction; blindness; skin disorder; psoriasis; kidney disease;
 KW arterial hypertension; pain syndrome; Alzheimer's disease; dementia;
 KW hydrocephalus; alopecia; baldness; cancer.
 OS Homo sapiens.
 XX
 PN WO200259152-A2.
 XX
 PD 01-AUG-2002.
 XX
 PR 26-OCT-2001; 2001WO-US050539.
 XX
 PR 26-OCT-2000; 2000US-0243568P.
 XX
 PR 25-OCT-2001; 2001US-00243568.
 XX
 PA (UVRQ) UNITV ROCKEFELLER.
 XX
 PI Liedtke W, Heller S, Hudspeth AJ, Friedman JW;
 XX WPI: 2002-599762/64.
 DR N-PSDB; ABB979489.
 PT Modulating mechanoreception or mechanosensation, for diagnosing,
 PT preventing or treating e.g. hearing disorders, HIV or obesity, comprises
 PT administering a vanilloid receptor-related osmotically activated channel
 PT polypeptide.

XX Claim 2; Fig 2; 154pp; English.

XX The invention relates to modulating mechanoreception/mechanosensation in

CC a mammal by administering a vanilloid receptor-related osmotically

CC activated channel (VR-OAC) polypeptide, its active fragments or portions,

CC or by introducing a nucleic acid vector capable of expressing the VR-OAC

CC polypeptide. The method of the invention is useful for modulating

CC mechanoreception or mechanosensation, for diagnosing, preventing or

CC treating e.g. hearing disorders, Human Immunodeficiency virus (HIV),

CC obesity, vertigo of labyrinthine origin including motion sickness,

CC neurological disorders including ataxia, male infertility, immune

CC dysfunction, diabetes mellitus, chronic obstructive lung disorder,

CC bronchial asthma, sexual dysfunction, blindness due to corneal or retinal

CC causes, or skin disorders including psoriasis. Other conditions include

CC arterial hypertension, kidney diseases, pain syndromes, Alzheimer's

CC disease and other dementias, hydrocephalus, alopecia, baldness and

CC cancer. The VR-OAC may be used in detecting or assessing osmotic and

CC mechanical stimuli, or as the facilitating component in translating an

CC osmotic or mechanical stimulus in nano-technological, biosensor or

CC bioborotic devices. The current sequence represents the amino acid

CC sequence of human VR-OAC as determined from HEK293 cells. NOTE: The

CC inventors indicate the presence of further VR-OAC polypeptides other than

CC those given in records AB98197-8. However, no sequence information

CC regarding these polypeptides which are referred to as SEQ ID's 5, 6, 7, 8

CC and 9 is given

XX

XX Sequence 871 AA.

Query Match 99.2%; Score 3828; DB 5; Length 871;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQSEPPRAGPGVAAELPGDESGTGGGAAPLSSLANLFGEGDGLSPSPADSRAPG 60
 DB 1 MAQSEPPRAGPGVAAELPGDESGTGGGAAPLSSLANLFGEGDGLSPSPADSRAPG 60
 QY 61 GDGRPNRMKFGQAFKGVNPIDLESTYESSVVPKPKAPMDSLFYGTYRHSSDN 120
 DB 61 GDGRPNRMKFGQAFKGVNPIDLESTYESSVVPKPKAPMDSLFYGTYRHSSDN 120
 QY 121 KRMKKTIIEKOPQSPKAPAPPPILKYFNRPILFDIVSRGSTADLDGLPLITHTKKRL 180
 DB 121 KRMKKTIIEKOPQSPKAPAPPPILKYFNRPILFDIVSRGSTADLDGLPLITHTKKRL 180
 QY 121 KRMKKTIIEKOPQSPKAPAPPPILKYFNRPILFDIVSRGSTADLDGLPLITHTKKRL 180
 DB 121 KRMKKTIIEKOPQSPKAPAPPPILKYFNRPILFDIVSRGSTADLDGLPLITHTKKRL 180
 QY 181 TDEEPRSPSGKTLCPALNLSNGRNDTIPVLDIARTGNMEEFINSFPRDIYYRGQT 240
 DB 181 TDEEPRSPSGKTLCPALNLSNGRNDTIPVLDIARTGNMEEFINSFPRDIYYRGQT 240
 QY 181 TDEEPRSPSGKTLCPALNLSNGRNDTIPVLDIARTGNMEEFINSFPRDIYYRGQT 240
 DB 181 TDEEPRSPSGKTLCPALNLSNGRNDTIPVLDIARTGNMEEFINSFPRDIYYRGQT 240
 QY 241 ALHAIERCKHYVELLYAAGADVHAQARGFPOPKDEGGYFYFGEPLSLIACTNOPHI 300
 DB 241 ALHAIERCKHYVELLYAAGADVHAQARGFPOPKDEGGYFYFGEPLSLIACTNOPHI 300
 QY 301 VNYITENPHKADNRQDSRGNTYLAHALVAADNTRENTKVTYMDLLKCARLPDS 360
 DB 301 VNYITENPHKADNRQDSRGNTYLAHALVAADNTRENTKVTYMDLLKCARLPDS 360
 QY 301 VNYITENPHKADNRQDSRGNTYLAHALVAADNTRENTKVTYMDLLKCARLPDS 360
 DB 301 VNYITENPHKADNRQDSRGNTYLAHALVAADNTRENTKVTYMDLLKCARLPDS 360
 QY 361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIRREVDETRHLSKFKDMAYGPVSSLYD 420
 DB 361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIRREVDETRHLSKFKDMAYGPVSSLYD 420
 QY 361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIRREVDETRHLSKFKDMAYGPVSSLYD 420
 DB 361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIRREVDETRHLSKFKDMAYGPVSSLYD 420
 QY 421 LSSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLDKMKKRGAVSYINVSYL 480
 DB 421 LSSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLDKMKKRGAVSYINVSYL 480
 QY 421 LSSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLDKMKKRGAVSYINVSYL 480
 DB 421 LSSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLDKMKKRGAVSYINVSYL 480
 QY 481 AMVFTLTAYYQPLEGTPPYPRITVDYLRLAGVITLFTGVLTFPTNLIKLEMKKCGV 540
 DB 481 AMVFTLTAYYQPLEGTPPYPRITVDYLRLAGVITLFTGVLTFPTNLIKLEMKKCGV 540
 QY 481 AMVFTLTAYYQPLEGTPPYPRITVDYLRLAGVITLFTGVLTFPTNLIKLEMKKCGV 540
 DB 481 AMVFTLTAYYQPLEGTPPYPRITVDYLRLAGVITLFTGVLTFPTNLIKLEMKKCGV 540
 QY 541 NSLFDGSGFOLLFYFYSVLIVSALYLAGIETAYLAWVAFVLCMMNALYFTRGKLKG 600
 DB 541 NSLFDGSGFOLLFYFYSVLIVSALYLAGIETAYLAWVAFVLCMMNALYFTRGKLKG 600

QY 601 TYSIMIOKILFKDLERFELLVILLPMIGVASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 DB 601 TYSIMIOKILFKDLERFELLVILLPMIGVASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 QY 661 RQSEFTSTLDDFKLTIGMDLEMSSSTKYPVFIILVYTIILFVLLNMLLMGE 720
 DB 661 RQSEFTSTLDDFKLTIGMDLEMSSSTKYPVFIILVYTIILFVLLNMLLMGE 720
 QY 721 TWGVSKESKHIMKLQ 736
 DB 721 TWGVSKESKHIMKLQ 736

RESULT 14
 AD181590 standard; protein; 871 AA.
 ID AD181590
 XX
 AC AD181590;
 XX
 DT 22-APR-2004 (first entry)
 XX
 XX Human vanilloid receptor-related channel protein #1.
 DE
 XX Human; calcium entry modulator; CD4536; CG5842; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.
 XX
 OS Homo sapiens.
 XX
 PN US2004009537-A1.
 XX
 PD 15-JAN-2004.
 XX
 PE 13-JAN-2003; 2003US-00342844.
 XX
 PR 11-JAN-2002; 2002US-0347459P.
 PR 02-AUG-2002; 2002US-040171P.
 PR 20-AUG-2002; 2002US-0405678P.
 XX
 PA (ROOS/) ROOS J.
 PA (STAU/) STAUDERMAN K.
 PA (VELI/) VELICELEBI G.
 XX
 PI Roos J, Stauderman K, Velicelebi G;
 XX
 DR WPI: 2004-090465/09.
 DR N-PSDB; AD181589.
 XX
 PT Identifying an agent that modulates intracellular calcium levels, useful
 PT for treating diseases associated with calcium dysregulation (e.g.
 PT cancer), comprises monitoring the effects of the agent on store-operated
 PT calcium entry.
 XX
 PS Disclosure; SEQ ID NO 60; 55pp; English.

XX The invention relates to identifying an agent that modulates

CC intracellular calcium comprising monitoring the effects of the agent on

CC store-operated calcium entry comprising contacting one or more test cells

CC or their portion comprising one or more proteins that is (are) at least

CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or

CC CG5842 over at least about 40% of the encoded protein (and that provides

CC for store-operated calcium entry with a test agent), where the portion of

CC the cell comprises the proteins, monitoring the effect(s) of the test

CC compound on store-operated calcium entry and identifying a test agent as

CC an agent if it has an effect on store-operated calcium entry

CC (comprising modulating the level of, expression of, activity of or

CC molecular interactions of a protein in a cell that has altered store-

CC operated calcium entry, where the protein is at least about 35%

CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842

CC over at least about 40% of the encoded protein and that provides for

CC store-operated calcium entry, and where store-operated calcium transport

CC into the cell is modulated) and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC AD181644 and AD181645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 XX

Sequence 871 AA;

Query Match 99.2%; Score 3828; DB 8; Length 871;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFEGBDGLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFEGBDGLSPSPADASRPAGP 60
QY 61 GGGPRLNRMKFGAERKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHSSDN 120
DB 61 GGGPRLNRMKFGAERKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHSSDN 120
QY 121 KMRKKITTEKOPSPAPAPOPPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 180
DB 121 KMRKKITTEKOPSPAPAPOPPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 180
QY 181 TDEEREPEPTGKTCPLKALINLSNGRNDTIPVLLDIAEKGMMREPIINSPPDIYRGQT 240
DB 181 TDEEREPEPTGKTCPLKALINLSNGRNDTIPVLLDIAEKGMMREPIINSPPDIYRGQT 240
QY 241 ALHIAIERCKAYVELVAQADVAHQARFFQPKDEGGYFYFGLPLSLAATNQPHI 300
DB 241 ALHIAIERCKAYVELVAQADVAHQARFFQPKDEGGYFYFGLPLSLAATNQPHI 300
QY 241 ALHIAIERCKAYVELVAQADVAHQARFFQPKDEGGYFYFGLPLSLAATNQPHI 300
DB 241 ALHIAIERCKAYVELVAQADVAHQARFFQPKDEGGYFYFGLPLSLAATNQPHI 300
QY 301 VVYLLENPKKADNRQDSRGNTVLAVALADNTRNTKPTKATYDLILKCARLPDS 360
DB 301 VVYLLENPKKADNRQDSRGNTVLAVALADNTRNTKPTKATYDLILKCARLPDS 360
QY 301 VVYLLENPKKADNRQDSRGNTVLAVALADNTRNTKPTKATYDLILKCARLPDS 360
DB 301 VVYLLENPKKADNRQDSRGNTVLAVALADNTRNTKPTKATYDLILKCARLPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTGKIGFOHITRREVTDEDETRHLSRKKDWAQPVYSLYD 420
DB 361 NLEAVLNNDGSLPLMAAKTGKIGFOHITRREVTDEDETRHLSRKKDWAQPVYSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILDRKRRFGAVSYINVSYL 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILDRKRRFGAVSYINVSYL 480
QY 481 AMVITLTAAYOPLGTPPYPRRTVDYKRLAGEVITLFTGLPFPFTINIKDLPMKKCRGV 540
DB 481 AMVITLTAAYOPLGTPPYPRRTVDYKRLAGEVITLFTGLPFPFTINIKDLPMKKCRGV 540
QY 541 NSLFIIDGSGFOLLFYFYSVLAISALYLAGIAYLAVMVFAVLGMNALYTRGLKLTG 600
DB 541 NSLFIIDGSGFOLLFYFYSVLAISALYLAGIAYLAVMVFAVLGMNALYTRGLKLTG 600
QY 601 TYSIMIQKILFEDLRFLLVYLLEMIIGYASALVSLNFCANMKVCNEDQNTCTVYTESC 660
DB 601 TYSIMIQKILFEDLRFLLVYLLEMIIGYASALVSLNFCANMKVCNEDQNTCTVYTESC 660
QY 661 RDSSEFSTFLDLFLKLTGMDLEMLSTKYPVVITLILVYITLFTVLLNMLIALMGE 720
DB 661 RDSSEFSTFLDLFLKLTGMDLEMLSTKYPVVITLILVYITLFTVLLNMLIALMGE 720
QY 721 TVGQVSKESKHIWKLO 736
DB 721 TVGQVSKESKHIWKLO 736

```

RESULT 15

ID ADE08372 standard; protein; 970 AA.

XX ADE08372;

DT 29-JAN-2004 (first entry)

DE Novel protein (useful for identifying genetic disorders) #527.

XX novel gene; novel protein; tissue marker; molecular weight marker;

KW chromosome marker; genetic disorder.

XX Unidentified.

OS WO2003054152-A2.

PN 03-JUL-2003.

PD 10-DEC-2002; 2002WO-US039555.

PF 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 14-MAR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372615P.

PR 12-APR-2002; 2002US-0012855P.

PR 24-APR-2002; 2002US-0376045P.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Wang G, Zhou P, Dymnac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

PI WPI; 2003-569235/53.

DR N-PSDB; ADE07461.

PT New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

PS Claim 20; SEQ ID NO 1438; 1177bp; English.

XX The invention comprises the amino acid and coding sequences of novel

XX proteins. The DNA and protein sequences of the invention are useful as:

XX markers for tissues in which the corresponding protein is preferentially

XX expressed; as molecular weight markers on gels; as chromosome markers or

XX tags; to identify chromosomes or to map related gene positions; and to

XX compare with endogenous DNA sequences in patients to identify potential

XX genetic disorders. The present amino acid sequence represents a protein

XX of the invention.

Sequence 970 AA;

Query Match 99.2%; Score 3828; DB 7; Length 970;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFEGBDGLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFEGBDGLSPSPADASRPAGP 159
QY 100 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFEGBDGLSPSPADASRPAGP 159
DB 100 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFEGBDGLSPSPADASRPAGP 159
QY 61 GGGPRLNRMKFGAERKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHSSDN 120
DB 61 GGGPRLNRMKFGAERKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHSSDN 219
QY 160 GGGPRLNRMKFGAERKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHSSDN 219
DB 160 GGGPRLNRMKFGAERKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHSSDN 219
QY 121 KMRKKITTEKOPSPAPAPOPPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 180
DB 121 KMRKKITTEKOPSPAPAPOPPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 279

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QY 181 TDEEFREPSTGKTCLPKALINLSNGRNDIIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
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Db 280 TDEEFREPSTGKTCLPKALINLSNGRNDIIPVLLDIAERTGNMREFINSPFRDIYYRGQT 339
    |||||
QY 241 ALHIAIERCKHYVELLVAGADVAQAQGRFPQPDGEGYFYGELPLSLAAGTNOBPHI 300
    |||||
Db 340 ALHIAIERCKHYVELLVAGADVAQAQGRFPQPDGEGYFYGELPLSLAAGTNOBPHI 399
    |||||
QY 301 VNYLTENPKKADMRKODSRGNTVLAVALADNTRENTKFTYKMDLLILKCARLFPDS 360
    |||||
Db 400 VNYLTENPKKADMRKODSRGNTVLAVALADNTRENTKFTYKMDLLILKCARLFPDS 459
    |||||
QY 361 NLEAVLNDGSLPLMAAATGKIIFOHIIIRREVDETRHLSRKTCDWAGPYSSLYD 420
    |||||
Db 460 NLEAVLNDGSLPLMAAATGKIIFOHIIIRREVDETRHLSRKTCDWAGPYSSLYD 519
    |||||
QY 421 LSLDTCGSEASVLELIVNSKIENHHEMLAVEPINELLDKMRKFGAVSFYINVSYL 480
    |||||
Db 520 LSLDTCGSEASVLELIVNSKIENHHEMLAVEPINELLDKMRKFGAVSFYINVSYL 579
    |||||
QY 481 AMVIFTLTAYYOPLBEGTPPYRYRTVDYRLAGEVITLFTGVLPFFTNIKDLFMKKCPGV 540
    |||||
Db 580 AMVIFTLTAYYOPLBEGTPPYRYRTVDYRLAGEVITLFTGVLPFFTNIKDLFMKKCPGV 639
    |||||
QY 541 NSLFIIDGSPQLYFIYSVLIVISALYLAGIEAYLAVMPFALVGMNNAIYFTRGKLTG 600
    |||||
Db 640 NSLFIIDGSPQLYFIYSVLIVISALYLAGIEAYLAVMPFALVGMNNAIYFTRGKLTG 699
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QY 601 TYSIMIQKILFKDLFRPLVYLLFMIGYASALVSLNPGANMKVCNEDQNCVPTYPSC 660
    |||||
Db 700 TYSIMIQKILFKDLFRPLVYLLFMIGYASALVSLNPGANMKVCNEDQNCVPTYPSC 759
    |||||
QY 661 RDSEFTSTFLDLFKLTIKMDLEMLSTKYPVVFIIILVTYIILTFVLLNMLIALMGE 720
    |||||
Db 760 RDSEFTSTFLDLFKLTIKMDLEMLSTKYPVVFIIILVTYIILTFVLLNMLIALMGE 819
    |||||
QY 721 TVGQVSKSKHIMKIQ 736
    |||||
Db 820 TVGQVSKSKHIMKIQ 835
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Search completed: December 2, 2004, 22:23:18
 Job time : 168 secs

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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:20:35 ; Search time 41 Seconds

(Without alignments)
1200.194 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSSGPRAGGEVAELPG.....GVVSKSKHIMKLQSGRRRL 742

Scoring table: BIOSUM62
Gapco 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	4	US-09-500-123-12
2	3823	99.1	871	4	US-09-500-123-7
3	3470	89.9	811	4	US-09-500-123-9
4	1604.5	41.6	843	3	US-09-235-451-25
5	1604.5	41.6	843	3	US-09-235-451-25
6	1579.5	40.9	838	4	US-09-235-451-2
7	1579.5	40.9	838	4	US-09-132-316-3
8	1579.5	40.9	838	4	US-09-667-422-9
9	1579.5	40.9	838	4	US-09-978-303-2
10	1579.5	40.9	839	3	US-09-197-636-2
11	1556.5	40.3	839	3	US-09-197-636-8
12	1556.5	40.3	839	3	US-09-235-451-34
13	1556.5	40.3	839	3	US-09-978-303-4
14	1555.5	40.3	839	4	US-09-533-220A-2
15	1552.5	40.2	839	3	US-09-197-636-4
16	1551.5	40.2	839	3	US-09-667-422-9
17	1551.5	40.2	839	3	US-09-978-303-2
18	1324	34.3	761	4	US-09-235-451-4
19	1306	33.9	761	4	US-09-978-303-4
20	1298.5	33.7	764	3	US-09-132-316-2
21	1298.5	33.7	764	3	US-09-235-451-36
22	1071	27.8	511	4	US-09-978-303-36
23	777	20.1	727	4	US-09-667-422-5
24	777	20.1	727	4	US-09-235-451-23
25	733	19.0	727	4	US-09-978-303-23
26	724.5	18.8	725	4	US-09-350-457A-2
27	548.5	14.2	279	4	US-09-149-476-500

28	227	5.9	71	3	US-09-235-451-14	Sequence 14, Appl
29	227	5.9	71	4	US-09-978-303-14	Sequence 14, Appl
30	221.5	5.7	1709	4	US-09-392-812A-6	Sequence 6, Appl1
31	210	5.4	1619	4	US-09-392-812A-4	Sequence 4, Appl1
32	180	4.7	1704	4	US-09-392-812A-2	Sequence 2, Appl1
33	172	4.5	1095	3	US-09-112-096-15	Sequence 15, Appl
34	172	4.5	1095	3	US-09-636-215-778	Sequence 778, App
35	172	4.5	1095	4	US-09-685-166A-778	Sequence 778, App
36	172	4.5	1095	4	US-09-679-426-778	Sequence 778, App
37	169	4.4	1095	4	US-09-636-215-780	Sequence 780, App
38	169	4.4	1095	4	US-09-685-166A-780	Sequence 780, App
39	169	4.4	1095	4	US-09-679-426-780	Sequence 780, App
40	155	4.0	1503	4	US-09-600-087-2	Sequence 2, Appl1
41	146	3.8	57	3	US-09-235-451-15	Sequence 15, Appl
42	146	3.8	57	3	US-09-978-303-15	Sequence 15, Appl
43	137	3.6	316	4	US-09-461-325-378	Sequence 378, App
44	137	3.6	316	4	US-10-012-542-378	Sequence 378, App
45	137	3.6	316	4	US-10-115-123-378	Sequence 378, App

ALIGNMENTS

RESULT 1	US-09-500-123-12	Sequence 12, Application US/09500123
Patent No. 6455278		
GENERAL INFORMATION:		
APPLICANT: Dublin, Adrienne E		
APPLICANT: Huvar, Arne		
APPLICANT: Erlander, Mark G		
APPLICANT: Glass, Charles A		
TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor		
FILE REFERENCE: Human VR3 receptors		
CURRENT APPLICATION NUMBER: US/09/500,123		
CURRENT FILING DATE: 2000-02-08		
NUMBER OF SEQ ID NOS: 17		
SOFTWARE: PatentIn Ver. 2.1		
SEQ ID NO 12		
LENGTH: 742		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-500-123-12		
Query Match	100.0%; Score 3858; DB 4; Length 742;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 742; Conservative	0; Mismatches	0; Gaps
0; Indels	0; Gaps	0;
QY	1	MADSSGPRAGGEVAELPGDESGTPGGRAPFLSIANLFEEDGSLSPADAPAP 60
DB	1	MADSSGPRAGGEVAELPGDESGTPGGRAPFLSIANLFEEDGSLSPADAPAP 60
QY	61	GGGRNLNMFQGAERKGVNPIDLESTLYSSVVPKPKAPMDLPDYGYRRHSSDN 120
DB	61	GGGRNLNMFQGAERKGVNPIDLESTLYSSVVPKPKAPMDLPDYGYRRHSSDN 120
QY	121	KMRKTIIEKQPSKAPAPPPPLIKVNNRILDIYRSSTADIDGLPLTHKKLU 180
DB	121	KMRKTIIEKQPSKAPAPPPPLIKVNNRILDIYRSSTADIDGLPLTHKKLU 180
QY	181	TDEPRESTGTCTPKALNLSNGRNPITPLTIAERTGMREPIINSPPFDIYRGQT 240
DB	181	TDEPRESTGTCTPKALNLSNGRNPITPLTIAERTGMREPIINSPPFDIYRGQT 240
QY	241	ALHIAIERCKHYVELVAQADVAQAGRFQPKDGGYFFGELPLSLAAGTNPRI 300
DB	241	ALHIAIERCKHYVELVAQADVAQAGRFQPKDGGYFFGELPLSLAAGTNPRI 300
QY	301	VNYLTENHKKADMRQDSRGVTHALVAIDNTRENTKPYTKYDILLKCAALFPDS 360
DB	301	VNYLTENHKKADMRQDSRGVTHALVAIDNTRENTKPYTKYDILLKCAALFPDS 360

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QY 361 NLEAVLNNDGLSPIMMAATGKIGIFQHIIRREVTDETRHLSRKEKDMAYGVVSSLYD 420
DB 361 NLEAVLNNDGLSPIMMAATGKIGIFQHIIRREVTDETRHLSRKEKDMAYGVVSSLYD 420
QY 421 LSLDTCGSEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
DB 421 LSLDTCGSEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
QY 481 AMVIFLTYAYOPLBEGPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
DB 481 AMVIFLTYAYOPLBEGPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
QY 541 NSLFDGSPQLLYFTISVLYSALYLAGIEAYLAWVPALVGMWNLAYFTRGKLTG 600
DB 541 NSLFDGSPQLLYFTISVLYSALYLAGIEAYLAWVPALVGMWNLAYFTRGKLTG 600
QY 601 TYSIMTOKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
DB 601 TYSIMTOKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
QY 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNMLALMGE 720
DB 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNMLALMGE 720
QY 721 TVGVSKESKHIMKLGSRRL 742
DB 721 TVGVSKESKHIMKLGSRRL 742

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RESULT 2
US-09-500-123-7
Sequence 7, Application US/09500123
Patent No. 6455278

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; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne B
; APPLICANT: Huyar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-7

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Query Match 99.1%; Score 3823; DB 4; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MADSSBGRAGPGEVAVELPGDESGTGGEARPLSLANLFGEDGSLSPSPADASRPAGP 60
DB 1 MADSSBGRAGPGEVAVELPGDESGTGGEARPLSLANLFGEDGSLSPSPADASRPAGP 60
QY 61 GDGPNTLMKQGAFRKGVNPIIDLESTLYESSVVPKKAAMDLSFDYGTYRHSSDN 120
DB 61 GDGPNTLMKQGAFRKGVNPIIDLESTLYESSVVPKKAAMDLSFDYGTYRHSSDN 120
QY 121 KRMKKITIEKQPSKAPAPQPPPLIKVFNPIIFDIYSRSTADLDGLLFPLLTHKKRL 180
DB 121 KRMKKITIEKQPSKAPAPQPPPLIKVFNPIIFDIYSRSTADLDGLLFPLLTHKKRL 180
QY 181 TDEFRRESTGKTLCPKALNLSNGRNDTIVLIDIAERTNGMEFINSPPRDIIYRGQT 240
DB 181 TDEFRRESTGKTLCPKALNLSNGRNDTIVLIDIAERTNGMEFINSPPRDIIYRGQT 240
QY 241 ALHAIERCKHYVELLVAQADVHAQARGFPQKDGCGYFPEELSLAACNQHPI 300
DB 241 ALHAIERCKHYVELLVAQADVHAQARGFPQKDGCGYFPEELSLAACNQHPI 300

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DB 241 ALHAIERCKHYVELLVAQADVHAQARGFPQKDGCGYFPEELSLAACNQHPI 300
QY 301 VNYLTENPKKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDLILKCARLPDS 360
DB 301 VNYLTENPKKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDLILKCARLPDS 360
QY 361 NLEAVLNNDGLSPIMMAATGKIGIFQHIIRREVTDETRHLSRKEKDMAYGVVSSLYD 420
DB 361 NLEAVLNNDGLSPIMMAATGKIGIFQHIIRREVTDETRHLSRKEKDMAYGVVSSLYD 420
QY 421 LSLDTCGSEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
DB 421 LSLDTCGSEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
QY 481 AMVIFLTYAYOPLBEGPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
DB 481 AMVIFLTYAYOPLBEGPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
QY 541 NSLFDGSPQLLYFTISVLYSALYLAGIEAYLAWVPALVGMWNLAYFTRGKLTG 600
DB 541 NSLFDGSPQLLYFTISVLYSALYLAGIEAYLAWVPALVGMWNLAYFTRGKLTG 600
QY 601 TYSIMTOKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
DB 601 TYSIMTOKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
QY 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNMLALMGE 720
DB 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNMLALMGE 720
QY 721 TVGVSKESKHIMKLG 736
DB 721 TVGVSKESKHIMKLG 736

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RESULT 3
US-09-500-123-9
Sequence 9, Application US/09500123
Patent No. 6455278

```

; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne B
; APPLICANT: Huyar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-9

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Query Match 89.9%; Score 3470; DB 4; Length 811;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 675; Conservative 0; Mismatches 1; Indels 60; Gaps 1;

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DB 1 MADSSBGRAGPGEVAVELPGDESGTGGEARPLSLANLFGEDGSLSPSPADASRPAGP 60
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DB 61 GDGPNTLMKQGAFRKGVNPIIDLESTLYESSVVPKKAAMDLSFDYGTYRHSSDN 120
QY 121 KRMKKITIEKQPSKAPAPQPPPLIKVFNPIIFDIYSRSTADLDGLLFPLLTHKKRL 180
DB 121 KRMKKITIEKQPSKAPAPQPPPLIKVFNPIIFDIYSRSTADLDGLLFPLLTHKKRL 180
QY 181 TDEFRRESTGKTLCPKALNLSNGRNDTIVLIDIAERTNGMEFINSPPRDIIYRGQT 240
DB 181 TDEFRRESTGKTLCPKALNLSNGRNDTIVLIDIAERTNGMEFINSPPRDIIYRGQT 240
QY 241 ALHAIERCKHYVELLVAQADVHAQARGFPQKDGCGYFPEELSLAACNQHPI 300
DB 241 ALHAIERCKHYVELLVAQADVHAQARGFPQKDGCGYFPEELSLAACNQHPI 300

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Qy 181 TDEFRPSTGKTCPLPALLNLNGRNDTTPVLLDIAERTGNMREPTNSPRDIYRGQT 240
Db 181 TDEFRPSTGKTCPLPALLNLNGRNDTTPVLLDIAERTGNMREPTNSPRDIYRGQT 240
Qy 241 ALHAIERRCHGYVELLVAOGADVHAOARGFPQKQGGYFYGELPLSLAATGNPHI 300
Db 241 ALHAIERRCHGYVELLVAOGADVHAOARGFPQKQGGYFYGELPLSLAATGNPHI 300
Qy 301 VNYITENPHKKADNRRODSRGNTVLAHALVADNTRENTKFTVMYDLLLKCARLPDPS 360
Db 301 VNYITENPHKKADNRRODSRGNTVLAHALVADNTRENTKFTVMYDLLLKCARLPDPS 360
Qy 361 NLEAVLNNDGLSPILMAAKTGKIGI FQHIIRREVTDEDTYHLSRKFQMAVGPVYSSLYD 420
Db 361 NLEAVLNNDGLSPILMAAKTGKIGI FQHIIRREVTDEDTYHLSRKFQMAVGPVYSSLYD 420
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVPEINELLRDKMRKFGAVSFYINVSYL 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVPEINELLRDKMRKFGAVSFYINVSYL 480
Qy 481 AMVIFLLTAYYQPLEGTPPYRTVDYRLAGBVLTLFTGVLFPTNIDLFMKKCPGV 540
Db 481 AMVIFLLTAYYQPLEGTPPYRTVDYRLAGBVLTLFTGVLFPTNIDLFMKKCPGV 540
Qy 541 NSLFTDGSFOLYFETSVLYSVAALYAGIENYLAVMVAVLVGMNALYFTRGLKLTG 600
Db 541 NSLFTDGSFOLYFETSVLYSVAALYAGIENYLAVMVAVLVGMNALYFTRGLKLTG 600
Qy 601 TVSIMIOKILFKDLFRFLVLYLLFMIGYASALVSLPNCANMVCNEDQNCVPPYPSG 660
Db 601 TVSIMIOKILFKDLFRFLVLYLLFMIGYASALVSLPNCANMVCNEDQNCVPPYPSG 660
Qy 661 ROSEFTSTFLDLFKLTIGMDLEMLSTKYPVFIILVYIILFTVLLNMLALMGE 720
Db 661 ROSEFTSTFLDLFKLTIGMDLEMLSTKYPVFIILVYIILFTVLLNMLALMGE 720
Qy 721 TVGVSKESKHIMKIQ 736
Db 721 TVGVSKESKHIMKIQ 736
Qy 736 TVGVSKESKHIMKIQ 736
Db 736 TVGVSKESKHIMKIQ 736

```

```

RESULT 4
US-09-235-451-25
; Sequence 25, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 843
; TYPE: PRT
; ORGANISM: chicken
; US-09-235-451-25

```

```

Query Match 41.6%; Score 1604.5; DB 3; Length 843;
Best Local Similarity 47.5%; Pred. No. 1.2e-143;
Matches 343; Conservative 128; Mismatches 184; Indels 67; Gaps 18;
Db 27 DGBSAL-ETAD-----NIOGT-----SKVOPSKSNITARRGRFWG 64

```

```

Qy 99 ---PKAPMDSLEPY-----GTYRHSSDNKMRKKTIEKOP---QSPKAPAPQPPIL 146
Db 65 DCDKMAAPMDSFYOMDHLAPSVIKFPAANMERKGLHLLSTDSITGCSERA-----F 116
Qy 147 KVNRPILFDIVSRGSTDADGLLPFLTLTKKRLTDEFRPSTGKTCPLPALLNLNGR 206
Db 117 KFYDRRIIDFAVARGSTKDDLLLYNLRLKHLTDDEFEPETGKTCPLKAMLNLDGK 176
Qy 207 NDTIPLVLLDIAERTGNMREPTNSPRDIYRGQTALHAIERRCHGYVELLVAOGADVHA 266
Db 177 NDTIPLVLLDIAERTGNMREPTNSPRDIYRGQTALHAIERRCHGYVELLVAOGADVHA 266
Qy 267 QARGFPQKQGGYFYGELPLSLAATGNPHIYNYITENPHKKADNRRODSRGNTV 325
Db 237 QARGFPQKQGGYFYGELPLSLAATGNPHIYNYITENPHKKADNRRODSRGNTV 325
Qy 326 HALVADNTRENTKFTVMYDLLLKCARLPDPSNLEAVLNNDGLSPILMAAKTGKIGI 385
Db 296 HALVADNTRENTKFTVMYDLLLKCARLPDPSNLEAVLNNDGLSPILMAAKTGKIGI 385
Qy 386 FQHIIRREVTDEDTYHLSRKFQMAVGPVYSSLYDLSLDTGGEASVLEILVYNSKIEN 445
Db 356 FQHIIRREVTDEDTYHLSRKFQMAVGPVYSSLYDLSLDTGGEASVLEILVYNSKIEN 445
Qy 446 RHEMLAVPEINELLRDKMRKFGAVSFYINVSYLCAVFTLTAAYQPLE--GTPPYPY-- 502
Db 415 RHEMLAVPEINELLRDKMRKFGAVSFYINVSYLCAVFTLTAAYQPLE--GTPPYPY-- 502
Qy 503 RTTVLYRLAGBVLTLFTGVLFPTNIDLFMKKCPGVNSLFTDGSFOLYFETSVLYV 562
Db 475 HSTGEYFRYTGELISVGLYFFFRIGQ-YFVQRRSLKTLIYDSISVLYFVHSLILS 533
Qy 563 SVALYAGIENYLAVMVAVLVGMNALYFTRGLKLTGYSIMIOKILFKDLFRFLVLY 622
Db 534 SVALYAGIENYLAVMVAVLVGMNALYFTRGLKLTGYSIMIOKILFKDLFRFLVLY 622
Qy 623 LFMIGYASALVSLPNCANMVCNEDQ--NCTVPPYPSGRDSTST-----FLIDF 674
Db 594 VILGFSTAVVTLIED-----DNGQDQNTSS--EYARSHRKGRGTSYNSLYTCTE 645
Qy 675 KLTIGMDLEMLSTKYPVFIILVYIILFTVLLNMLALMGEYGVSKESKHIMK 734
Db 646 KLTIGMDLEMLSTKYPVFIILVYIILFTVLLNMLALMGEYGVSKESKHIMK 705
Qy 735 LQ 736
Db 706 LQ 707

```

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RESULT 5
US-09-978-303-25
; Sequence 25, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsacin receptor and capsacin receptor-related
; FILE REFERENCE: UCA1084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25

```

LENGTH: 843
 TYPE: PRF
 ORGANISM: chicken
 US-09-978-303-25

Query Match
 Best Local Similarity 47.5%; Pred. No. 1.2e-143;
 Matches 343; Conservative 128; Mismatches 184; Indels 67; Gaps 18;

QY 41 EGDGSLSPADAPAGDGRPNLRKFGAFKGVNPIIDLESTLY--ESSVPG 98
 DB 27 DGDSDAL--ETAD-----NLQSTF-----SNKQPSKSNIPARGFVWG 64
 QY 99 ---PKRPMDSLDY-----GTYRHSSDNKRMRKKIIEKCP---QSPAPAPQPPILI 146
 DB 65 DCDKMAWPDSPQOMHLMAPSVIKFHANERGLKHLSTDSITGCSERA-----F 116
 QY 147 KVENREPLPDIVSRGSTADLDGLLPILLTHKKQLTDEEPREPSTGKTCIPKALINLSGR 206
 DB 117 KEVDRRIRFDVARGSTKDLDDLILYINRLTKHLTDDEFKPEPTGKTCIKAMLNHDGK 176
 QY 207 NDIPPLLDIAETGMMREINSPRDIYRSGOTAHIAIERCKHYVELLVAQADVHA 266
 DB 177 NDIPPLLDIAETGKTLKEFVNAEYTDNYKGTALHIAERKMTLVKLVQADVHA 236
 QY 267 QARGRFQF--KDEGQYFEGELPLSLAAGTNPPIVNYLTENPHKADMRSDRGNTVL 325
 DB 237 RAGEFFRRTKKGKPG--FYFGEPLSLAAGTNPCTIVFLEENPYQADIAEDSMGMVVL 295
 QY 326 HALVAIDNTRENTKPVTKMYDLILKCARLPDPSNLEAVLNDGLSPMLMAAKTGICGI 365
 DB 296 HTLVEIADNTKMTKFTVKMYNNILILGAKINPILKLEELTNKKGLPLTLAAKTGKIGI 355
 QY 386 FOHIIREVDEDETRHLSRKFQMAVGVYSLSYDLSLDTGCEASVLEILVNSKLEN 445
 DB 356 FAYILREIADPEGRHLSRKFTEWAGPVHSLDLSCTDTC--EKNSVLEIAYSSSTPN 414
 QY 446 RHEMLAVEPINELLDKMRKGAVSFYINVSYLCAWVIFLTAVYQPLR--GTPPYVY- 502
 DB 415 RHEMLAVEPINRLLODKMDRVRKHLFFNFVVAIHLISLTAVYRVPVQGDPRPAFG 474
 QY 503 RTIVDYLRAGEVITLFTGVLPFTTNIKDLFMKCCPGVNSLFDGSQLYFISVVIY 562
 DB 475 HSTGEYFRVGEILSYGVGLTFEPPRGIO--YVQRRPSIKTLIVDSYSEVLEFVHSLILLS 533
 QY 563 SAALYIAGIEIYAVMVFALVGMNALLYFRGLKLGIVSIMOKLIFKDLFFELLYVL 622
 DB 534 SVVLYFCQGLYVAMVFSIALGMANMLYTRGFQMGIVSVMLAKILRDLCRFMEVYL 593
 QY 623 LFMIGVASALVSLNPCANMKVCNEDQ--TNCVPTVPSCRDSETFST-----FLIDLF 674
 DB 594 VFLIGFSAVYLTLED-----DNEGQDTNS--EYARCSHTKRGRTSYNSLYTCELEF 645
 QY 675 KLITGMGDELMSTKYPVFIILLYIITFVLLNMLIALMGETGVGSXSKSHIWK 734
 DB 646 KFTIGMGDLFETENYRKSVEFVILLYVILLYIILNMLIALMGETVSKIAQSKSIWK 705
 QY 735 LQ 736
 DB 706 LQ 707

RESULT 6
 US-09-235-451-2
 Sequence 2, Application US/09235451

GENERAL INFORMATION:
 APPLICANT: Julius, David J.
 APPLICANT: Caterina, Michael J.
 APPLICANT: Brake, Anthony J.
 TITLE OF INVENTION: NICOTIC ACID SEQUENCES ENCODING
 TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
 TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
 FILE REFERENCE: 9076/084CIP

CURRENT APPLICATION NUMBER: US/09/235,451
 CURRENT FILING DATE: 1999-01-22
 PRIOR APPLICATION NUMBER: 60/072,151
 PRIOR FILING DATE: 1998-01-22
 PRIOR APPLICATION NUMBER: 08/915,461
 PRIOR FILING DATE: 1997-08-20
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 838
 TYPE: PRF
 ORGANISM: R. rattus
 US-09-235-451-2

Query Match
 Best Local Similarity 40.9%; Score 1579.5; DB 3; Length 838;
 Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

QY 16 AELPGRBSGTPGGE-----AFPLSLANLPEGEDGSLSPADADA 54
 DB 5 ASIDSESSSPQENSCLDPPDRDPNCKPPYKPHIFTRSRKTRLF--GKGDSEASPLDC 63
 QY 55 SRPAGGDRGNLRMRKFGAFKGVN--PIDLESTLYESSVVPGEKAPMDSLFDYGYI 113
 DB 64 PYREG-----GLASCPILTVSVL-----TIQPGDGP-----ASV 94
 QY 114 RHHSNKRMRKKIIEKQPSAPAPQPPILKVENRPIEDIVSRGSTADLDGLPFL 173
 DB 95 RPSQDS-----VSAGEKPP--RLVDRRSIFPAVAVQSNQCELESLEPL 136
 QY 174 LTHKKQLTDEEPREPSTGKTCIPKALINLSGRNDITPVLLDIAERTGNREINSPFRD 233
 DB 137 ORSKRLTDEEPREPSTGKTCIKAMLNHNGNDITALLDVARKDSLKQFVNASYTD 196
 QY 234 IYRGTALHIAIERCKHYVELLVAQADVHAQARGFPQDEGQYFPGELPLSLAA 293
 DB 197 SYKKGQALHIAIERRMNTLVTLVENGADVQAANDFFKTKGRPGFYFGEPLSLAA 256
 QY 294 CTNQPPIVNYLTENPHKADMRSDRGNTVLAHALVAIDNTENKFTVKMYDLILKLC 353
 DB 257 CTNOLAVKPELQNSWQPADISARDSVGNVTALVAEADNTVDNKFVSMNEIILIG 316
 QY 354 ARLEPDSNLEAVLNDGLSPMLMAAKTGICIGFOHIIREVDEDETRHLSRKFQMAVGP 413
 DB 317 AKHPLTKLEITTRKGLTPALAASSGKIGVLAIIQRIHBECHLSKFTEMAYGP 376
 QY 414 VYSLYDLSLDTGCEASVLEILVY--NSKIENRHEMLAVEPINELLDKMRKGAVSFY 472
 DB 377 VHSLSYDLSCTDTC--EKNSVLEIAYSSSETPNHDMLVEPLNRLLODKMDRFEVKRTFY 435
 QY 473 INVVSYLCAWVIFLTAVYQPLEGTPPYKRTV--DYLRLAGEVITLFTGVLPFTTNIXD 531
 DB 436 FNFVYCIYMIIFTPAAVYRVEBGLPPYKLVNVDYFRVYGLTSLVSGGVYFEPGRIO-- 494
 QY 532 LFMKCCPGVNSLFDGSQLYFISVVIYSAALYIAGIEIYAVMVFALVGMNALLY 591
 DB 495 YFQRRBSKSLFDGSQLYFISVVIYSAALYIAGIEIYAVMVFALVGMNALLY 554
 QY 592 FTRGLKLGIVSIMOKLIFKDLFFELLYIILNMLIALMGETGVGSXSKSHIWK 651
 DB 555 YTRGFQMGIVAVMIEMKILRDLCRFMEVYLVFPGFSTAVVTLI-----EDGKN 604
 QY 652 CTVP-----TYPSCRDS-----ETFTPLLDLFKTLTGMGDELMSTKYPVFIIL 699
 DB 605 NSLPWESSTPHKCRGACKCPGANSYNSLYST--CLELFPKFTTIGGDLFETENYFKAIVFIIL 663
 QY 700 VTYIILFVLLNMLIALMGETGVGSXSKSHIWK 736
 DB 664 LAYILTYIILNMLIALMGETVKNIAQSKSHIWK 700

RESULT 7
 US-09-132-316-3

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; Sequence 3, Application US/09132316B
; Patent No. 6444440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1468.1110000
; CURRENT APPLICATION NUMBER: US/09/132.316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 838
; TYPE: PR
; ORGANISM: Rattus norvegicus
; US-09-132-316-3

```

```

Query Match      40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 3e-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

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16 AALPDESGTPEGE-----AFPLSLANLFEEDGSLSPADA 54
5 ASIDSESESPPOENSCLDPPDRDPCPKPPVPHFTTRSRTRLF-GKGDSEASPLDC 63
55 SRPAGGDRPVLAKMFGQAFKGVN-PIDLLESTLVSSVPGKAPMOSLFGYGY 113
64 PYERG-----GLASCPITVSVL-----TIQPGDGP-----ASV 94
114 RHSSDNKRWKRIIEKOPQSPKAPAPQPPILKVNRPILPDIYVRSSTADLGLPFL 173
95 RSSQDS-----VSAGEKP--RLYDRSIFDVAQNSCQELLESILPFL 136
174 LTHKRLTDEEREPSTGTCTCPKALLNSNGRNTIPLYLDIAERTGNMREFINSPPD 233
137 QRSKRLTDESEKDEPTGKTCILKMLNHNQNDITALLDVARKTSLKQFVNASYTD 196
234 IYRGQTALHIAIERCKHYVELVAQADVAHQAARGPFQKDGSGYYPGELPLSLAA 293
197 SYKQGTALHIAIERKNTLVTLLVENGADVAAGDFKTKGRPGFYFGBELPLSLAA 256
234 CTNPHIVNYLTENPHKADMRDGRGNTVLAHALVAADNTRENTKFTKYDILLK 353
257 CTNGLAIKFLQNSQPADISARDSVGNTVLAHALVEADNTVDNTKFTSYNNEILLIG 316
354 AALPDSNLEAVLNDGSLPMAAKTGIGIFOHITREVTDETRHLSRKFQWAGP 413
317 AKLHPTLKLERTNKGTLPLALASSGKIGVLAIVLQREIHPECRHLSRKFTEWAGP 376
414 VYSSLYDSSLDTCGEASVLEIIVY-NSKINREHMLAVEPINELEKMKKFGAVSY 472
377 VHSSTLYDSCIDTC-EKNSVLEIVAYSSSETPNRHMLVEPLNLLDQKMRFYKRIFY 435
473 INVSYLCAMVITLTAYQPLEGTPPYRTTV-DYRLAGEVITLFTGYLFFFTNID 531
436 FNEFYCYLMIFLTAAYRYPVEGLPYLTKNTVGDYRVTGHIISVSGGVFFFRGIC 494
532 LFMKCKPGVNSLFDGSPQLVLIYSVLAIVSALYAGIEAVLAVMYPALVGMNNALY 591
495 YFLGRPSIKSLFVDSSEILFFVQSLFVLVSVLVYFSORKEYVASWVFLMGMNTMLY 554
592 FTFGKLGTVSIMOKLIFLDFRFLVYLFLMIGVASALVSLNPPCANMKVCEDQTN 651
555 YTRGQMGITVAAMLEKMLRDLKRFMYIVLFLGFSIAVVTLL-----EDGN 604
652 CTVP---TYPSCRDS-----ETFTFLDLFLKLTIGMGDLMLSLTKYVAVFILL 699
605 NSLPWESIPHKCRGACCKPGNSVNSLST-CLFLKFTIIGMGDLFTENYDKAVFILL 663

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QY 700 VTYIILFVLLANMLALMGETVGOVSKESKHTMKLO 736
DB 664 LAIVILTYILLANMLALMGETVYKIAQESKNIMKLO 700

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RESULT 8
US-09-667-422-9
; Sequence 9, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PR
; ORGANISM: Rattus sp.
; PUBLICATION INFORMATION:
; AUTHORS: Caterina, Michael J.
; AUTHORS: Schumacher, Mark A.
; AUTHORS: Tomioka, Makoto
; AUTHORS: Rosen, Tobias A.
; TITLE: The capsaicin receptor: a heat-activated ion channel in
; JOURNAL: Nature
; VOLUME: 389
; PAGES: 816-824
; DATE: 1997
; US-09-667-422-9

```

```

Query Match      40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 3e-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

```

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16 AALPDESGTPEGE-----AFPLSLANLFEEDGSLSPADA 54
5 ASIDSESESPPOENSCLDPPDRDPCPKPPVPHFTTRSRTRLF-GKGDSEASPLDC 63
55 SRPAGGDRPVLAKMFGQAFKGVN-PIDLLESTLVSSVPGKAPMOSLFGYGY 113
64 PYERG-----GLASCPITVSVL-----TIQPGDGP-----ASV 94
114 RHSSDNKRWKRIIEKOPQSPKAPAPQPPILKVNRPILPDIYVRSSTADLGLPFL 173
95 RSSQDS-----VSAGEKP--RLYDRSIFDVAQNSCQELLESILPFL 136
174 LTHKRLTDEEREPSTGTCTCPKALLNSNGRNTIPLYLDIAERTGNMREFINSPPD 233
137 QRSKRLTDESEKDEPTGKTCILKMLNHNQNDITALLDVARKTSLKQFVNASYTD 196
234 IYRGQTALHIAIERCKHYVELVAQADVAHQAARGPFQKDGSGYYPGELPLSLAA 293
197 SYKQGTALHIAIERKNTLVTLLVENGADVAAGDFKTKGRPGFYFGBELPLSLAA 256
234 CTNPHIVNYLTENPHKADMRDGRGNTVLAHALVAADNTRENTKFTKYDILLK 353
257 CTNGLAIKFLQNSQPADISARDSVGNTVLAHALVEADNTVDNTKFTSYNNEILLIG 316
354 AALPDSNLEAVLNDGSLPMAAKTGIGIFOHITREVTDETRHLSRKFQWAGP 413
317 AKLHPTLKLERTNKGTLPLALASSGKIGVLAIVLQREIHPECRHLSRKFTEWAGP 376
414 VYSSLYDSSLDTCGEASVLEIIVY-NSKINREHMLAVEPINELEKMKKFGAVSY 472
377 VHSSTLYDSCIDTC-EKNSVLEIVAYSSSETPNRHMLVEPLNLLDQKMRFYKRIFY 435
473 INVSYLCAMVITLTAYQPLEGTPPYRTTV-DYRLAGEVITLFTGYLFFFTNID 531

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Db      436  FNFVYVCLIMIIETFAAYRPRBGLPYKLNKTVGDYFRTVBELLVSQGVYFFRGIO- 494
Qy      532  LFMKKCGVNSLFDIDSPOLLYFYISVLVYSAAALYAGIEAYLVAVPALVIGMNNALY 591
Db      495  YFLQRPRIKISLFPVDSYBILFEFVQSLFELVAVVLYYFSQRKEVAVSMVSLAGMNNMY 554
Qy      592  FTRGKLTGYSYIMIOKILFKDLFRFLLYVLLFMIGYAGALVSLNLPANMKVCNEDQTN 651
Db      555  YTRGQMGGIYAVMLEKXIMLRDLGRMFYIVLFLFBSYAVVLLI-----EDGKY 604
Qy      652  CTVP--TVPSGRDS-----ETFSFFLLDLFKLTIGMGDLMLSTKYVVFRTILL 659
Db      605  NSLIPESTPHKRCGACCKPGNSYNSLYSE-CLELFFRTIGMGDLFFETENYDFKAVFTILL 663
Qy      700  VTYILTFVILLNMLIALMGETVGVGSKSKHIMKIQ 736
Db      664  LAYVILTYILLNMLIALMGETVYVKNKAQSKHIMKIQ 700

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RESULT 9
US-09-978-303-2
; Sequence 2, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 838
; TYPE: PRT
; ORGANISM: R. rattus
US-09-978-303-2

```

```

Query Match Similarity 40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 36-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16

Qy 16 AELPDESGTPEG-----AFPLSLANLFEKGDGSLSPRADA 54
      : : : : :
Db 5 ASDSDSESPQENSCIDPPDRDPNCKPPVKPHIFTRSRTRLF-GKGDSEASPLDC 63
      : : : : :
Qy 55 SRPAGGDSRPILRMKPFQAFKKGVN-PTDLESTLYESSVCPGKKRPMDSLEDYGY 113
      : : : : :
Db 64 PYEEG-----GLASCTITVSSVL-----TIQRGDP-----ASV 94
      : : : : :
Qy 114 RHHSNNKMKRKIKLEKQPSKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPVL 173
      : : : : :
Db 95 RSSQDS-----VSAGEKRP-RLYDRRSIFDAVAQSNCOEIESLDPELT 136
      : : : : :
Qy 174 LTHKKRLTBEERPREPSTGKCLPKALLNSGNDPIPLVLDIAEKTAMREIRINSPFD 233
      : : : : :
Db 137 QRSKKRLTSEFPDPTGKTLCKLAKMLNHNQNDITALLDVAKTIDSLKQFVNASYTD 196
      : : : : :
Qy 234 IYRGGTALHIAIERRCRYVELLVNQADVHAQARGFPQKDEGGYVFGELPLSLAA 293
      : : : : :
Db 197 SYTKGCTALHIAIERNNMLLVTLVENGADVQAANGDPFKTKGARGFYFGLPLSLAA 256
      : : : : :
Qy 294 CTNQHPIVYLVLENPKADMRRODSRGNTVLAHVAIADNTRENTKFTYKMYDILLMC 353
      : : : : :

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Db      257 CTNOLAIVAFILONSGNPADISARBSVGVTVHALVEADTVDTKVTSMNYEILILG 314
Qy      354 ARLEPDSNLEAVLNDGSLPLMMAAKTKYIGIJOHIIREVTDEDTRLSKKFDMAKCP 413
      317 AKHLPTLKBEIINRKGTLPLLAASSGKIGVAVIIQREIHPEPCRHLSKRTFEMAYGP 376
Qy      414 VYSLYDLSLDTGCEASVLEIIV-NSKINRHEMLAVEINELLDKRRKKGAASEY 472
      377 VHSLSYDLSCTIDTC-EKNSVLEIVASSESETPNRDMLVPELNKLLQDKMDRVPKSI FY 435
Db      473 INVSYICAMVITFLTAYQPLEGTPPYRYRTV-DYLRAGEVTLFTGVLFPEFTNKD 531
Qy      436 FNEFVYCLYMIIFTLAAAYRPEVGEPLPYLKNVTGDPYRVGTSELISVSGVYFFERGIQ- 499
Db      532 LFMKCKGVNSLFIIDSFOLAVFIYSVLIVTSALYIAGIEAVLYAWFALVGMNATLY 591
      495 YFQRRPSLSLFDVDSYSELFEFVQSEFWLVSVLYFSQRKELYASWVFSIAMGHTMKLY 555
Qy      592 FTBGLKLTGYSIMIXIKI:::..:::..:::..:::..:::..:::..:::..:::.. 651
      555 YTRGFQMGYIAYAMIERKMLURDCRMFYVILPFGFSAVVTL-----EDGKN 604
Db      652 CTVP---TYPSCRDS-----EYFSFTLLDFLRTIGMGDLEMLSTKYPVVEFIILL 699
Qy      605 NSLPMESTPHKCKGSACKRGNISYLSYR-CLELFFFTIGMGDLEFTENYOPKAVFIILL 666
Db      700 VTYIILFTVLINMLTALMGEITVQSKESKHIIMKIQ 736
Qy      664 LAYVITLYIILINMLTALMGEITNKAQSSKNIMKIQ 700

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INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 839 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-197-636-2

Query Match 40.4%; Score 1557.5; DB 3; Length 839;
 Best Local Similarity 44.5%; Pred. No. 3,7e-139;
 Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

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QY 49 PSPADASRPAGGDDGRPNL-----RMKFG-----AFKGVNPDILLES--TLVSSV 95
DB 22 PDLIDGDPNSRPPPAKPOLSTAKSRTRLFGKGDSEAFVDCPHEGEIDSCPTIVSPV 81
QY 96 V-----PGPKAPMDSLFYGYTRHSSDNKMKRKIIIEKOPSPKAPAPPPPIIKVF 149
DB 82 ITIQRPDGGPTGARL-----LSQSVAASTEXTLRILY 113
QY 150 NRPIIDIVSRGSTADLDGLPPLLTHKKRLTDEEFPREPSTGKTCCLKALNLSGRNDT 209
DB 114 DRSIFEAVAQNCCODESLILFLQSKKHLTNEFKDPETGKTCCLKAMLNLDGQNTT 173
QY 210 IPIVLIDIAERTGNMREFFINSPPFDIYRGQTALHAIERRCKHYVELVAOGADVAOAR 269
DB 174 IPIVLEIARQDLSLKELVNASYDYSYKQGTALHAIERRNMLVTLVENGADVOAAAH 233
QY 270 GRFPQKDEGGYFYFGEIPLSLAAGTNOPIHIVNYLTENPHKADMRQDSRGNTVLAHV 329
DB 234 GDFEKKTKRPGFYFGEIPLSLAAGTNOPIHIVNYLTENPHKADMRQDSRGNTVLAHV 293
QY 330 AIADNTRENTKFTYKMYDILLKCARLPDSNLEAVLNNDGSLPMAAAKTKIGIFQHI 389
DB 294 EVADNTADNTKFTYKMYDILLKCARLPDSNLEAVLNNDGSLPMAAAKTKIGIFQHI 353
QY 390 IRREVTDDETRHLSRKFKOMAYGPVYSLSYDLSLDTGCEBASVLEILVY-NSKIENRHE 448
DB 354 IRRVTDDETRHLSRKFKOMAYGPVYSLSYDLSLDTGCEBASVLEILVY-NSKIENRHE 412
QY 449 MLAVEPINLELDDKMKRFGAVSFYINVSYLCAVIFTLTAYIQPLEGPPYPRYRTVDY 508
DB 413 MLAVEPINLELDDKMKRFGAVSFYINVSYLCAVIFTLTAYIQPLEGPPYPRYRTVDY 472
QY 509 IRLAGEVITLFTGVLEFFTNIKDLFMKCGPVNSLFDGSPOLIVFYISVLIVSAATL 568
DB 473 FRYVTGEIILSVLGIVYFFFRGLQ-YFLQRPSPSKTILFVDSYSEMLFFLOSLFMALIVLYF 531
QY 569 AGIEAYLAVMFALVIGMNNALYFTRGLKLTGTYSIMIQILFKDLFRFLVYLLFMIGY 628
DB 532 SHIKKEYVAVSMVFSLALGWTNMLYTRGFQMGIVYAMIEKMLIRDLCRMFFIYIFLEGF 591
QY 629 ASALVSLNPGCANMKVNCNEDQNCVPTV-----PSCRDSER-----PSTFLDLFK 675
DB 552 STAAVTLI-----EDGKNDLPSSESTSHRRNGPACRPDSSYNSLYST-CLIELFK 640
QY 676 LTIKGADLEMLSTKYPVVFILLVYIILFVLLINMLIAMEGTGVSSESKHIMYL 735
DB 641 FTIGGDLLEFTENYDFKAVFILLVYIILFVLLINMLIAMEGTGVSSESKHIMYL 700
QY 736 Q 736
DB 701 Q 701

```

RESULT 11

US-09-197-636-8
 ; Sequence 8, Application US/09197636
 ; Patent No. 6239267
 ; GENERAL INFORMATION:
 ; APPLICANT: DUCKWORTH, DAVID
 ; APPLICANT: HAYES, PHILIP

```

? APPLICANT: MEADOWS, HELEN
? APPLICANT: DAVIS, JOHN
? TITLE OF INVENTION: NOVEL COMPOUNDS
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Ratner & Prestia
? STREET: P.O. Box 980
? CITY: Valley Forge
? STATE: PA
? COUNTRY: US
? ZIP: 19482-0980
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/197,636
? FILING DATE: 23-NOV-1998
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: UK 9805137.8
? FILING DATE: 12-MAR-1998
? APPLICATION NUMBER: UK 9815791.0
? FILING DATE: 21-JUL-1998
? APPLICATION NUMBER: UK 9819278.4
? FILING DATE: 03-SEP-1998
? ATTORNEY/AGENT INFORMATION:
? NAME: Prestia, Paul F
? REGISTRATION NUMBER: 23,031
? REFERENCE/DOCKET NUMBER: GP-30075
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 601-407-0700
? TELEFAX: 610-407-0701
? TELEX: 846169
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 839 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-197-636-8

Query Match 40.3%; Score 1556.5; DB 3; Length 839;
Best Local Similarity 44.5%; Pred. No. 4,7e-139;
Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

QY 49 PSPADASRPAGGDDGRPNL-----RMKFG-----AFKGVNPDILLES--TLVSSV 95
DB 22 PDLIDGDPNSRPPPAKPOLSTAKSRTRLFGKGDSEAFVDCPHEGEIDSCPTIVSPV 81
QY 96 V-----PGPKAPMDSLFYGYTRHSSDNKMKRKIIIEKOPSPKAPAPPPPIIKVF 149
DB 82 ITIQRPDGGPTGARL-----LSQSVAASTEXTLRILY 113
QY 150 NRPIIDIVSRGSTADLDGLPPLLTHKKRLTDEEFPREPSTGKTCCLKALNLSGRNDT 209
DB 114 DRSIFEAVAQNCCODESLILFLQSKKHLTNEFKDPETGKTCCLKAMLNLDGQNTT 173
QY 210 IPIVLIDIAERTGNMREFFINSPPFDIYRGQTALHAIERRCKHYVELVAOGADVAOAR 269
DB 174 IPIVLEIARQDLSLKELVNASYDYSYKQGTALHAIERRNMLVTLVENGADVOAAAH 233
QY 270 GRFPQKDEGGYFYFGEIPLSLAAGTNOPIHIVNYLTENPHKADMRQDSRGNTVLAHV 329
DB 234 GDFEKKTKRPGFYFGEIPLSLAAGTNOPIHIVNYLTENPHKADMRQDSRGNTVLAHV 293
QY 330 AIADNTRENTKFTYKMYDILLKCARLPDSNLEAVLNNDGSLPMAAAKTKIGIFQHI 389
DB 294 EVADNTADNTKFTYKMYDILLKCARLPDSNLEAVLNNDGSLPMAAAKTKIGIFQHI 353
QY 390 IRREVTDDETRHLSRKFKOMAYGPVYSLSYDLSLDTGCEBASVLEILVY-NSKIENRHE 448

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QY 96 V-----PGPKKAPMDSLFYGYTRHSSDNKRWKIIIEKQSPAPAPQPPILKVF 149
DB 82 ITTIRPGDGPFGARL-----LSQSVAASTKRTLR 113
QY 150 NRPLIFIVSRGSTADIDGLLPULLTHKKRLTDEEPREPTGKTCPLKALINLSNGRND 209
DB 114 DRSIFBAVAVQNNCODLESLLFLQSKSKHLLTNEFPDPTGKTCCLKAMINLHDGQNTT 173
QY 210 IPLLDAERTGNMREFFINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 269
DB 174 IPLLDAERTGNMREFFINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 233
QY 270 GREFQPDGEGYFPGELPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 329
DB 234 GDEFFKTKGRPGFYFGLPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 293
QY 330 AIDNRENTKFTYKMYDLILKCARLPDSNLEAVINNDGLSPIMAAATGKIGIHOI 389
DB 294 EVADNTADNTKFTYKMYDLILKCARLPDSNLEAVINNDGLSPIMAAATGKIGIHOI 353
QY 390 IREVTDEDTRLSRKPKDWAYGVYSSLYDLSLDTGCEASVLEIIVY-NSKIERRHE 448
DB 354 LOREIOPEBCRHLSRKFTEWAYGVHSLYDLSLDTGCEASVLEIIVY-NSKIERRHE 412
QY 449 MAVEPINELLRKMRKFGAVSFYINVSYLCAVITFTLTAAYOPLGTPPYRYRTVDY 508
DB 413 MLVEPINELLRKMRKFGAVSFYINVSYLCAVITFTLTAAYOPLGTPPYRYRTVDY 472
QY 509 LRLAGEVITLFTGVLFPEFTNIDLFMKKCPGVNSLFDISGFLLYFYSVLVISAALYL 568
DB 473 FRTYGBLSLVGVSFFFRIGIQ-YFLORBSMKTLFVDSSEMLFLOSIFMLATVLYLF 531
QY 569 AGIEAVLAVWVFLVGMNVALYTRGLKLTGYTSIMIQKLEKDFRPLVLYLLFMIGY 628
DB 532 SHKEVYAVWVFLVGMNVALYTRGLKLTGYTSIMIQKLEKDFRPLVLYLLFMIGY 591
QY 629 ASALVSLNPCANMKVCNEDQNCVPTY-----PSCRDET-----FSTFLDLFK 675
DB 592 STAVVTLI-----EDGKNDSLPSESTSHRWGAPACRPDSSVNSLYST-CLELFX 640
QY 676 LITGMGDLMLSTKPYVFIILVYIITFVLLNMLIALMGFTVGVGSKESKRIWKL 735
DB 641 FTIGMDLEFTEYDFAVFIILVYIITFVLLNMLIALMGFTVGVGSKESKRIWKL 700
QY 736 Q 736
DB 701 Q 701

RESULT 14
US-09-533-220A-2
; Sequence 2, Application US/09533220A
; Patent No. 6406908
; GENERAL INFORMATION:
; APPLICANT: McIntyre, Peter
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/09/533,220A
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 1.30
; SEQ ID NO 2
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-220A-2

Query Match 40.3%; Score 1555.5; DB 4; Length 839;
Best Local Similarity 44.5%; Pred. No. 5.8e-139;
Matches 321; Conservative 137; Mismatches 189; Indels 74; Gaps 12;

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QY 49 PSPADASRAPAGGGRPNL-----RMKFG-----AFKGVNPIDLES--TLYSSV 95
DB 22 PDLUDGPNSRPPAPKQULSTAKSRTLFPGGSEEPVVDCHPEGBELSCPTITVSPV 81
QY 96 V-----PGPKKAPMDSLFYGYTRHSSDNKRWKIIIEKQSPAPAPQPPILKVF 149
DB 82 ITTIRPGDGPFGARL-----LSQSVAASTKRTLR 113
QY 150 NRPLIFIVSRGSTADIDGLLPULLTHKKRLTDEEPREPTGKTCPLKALINLSNGRND 209
DB 114 DRSIFBAVAVQNNCODLESLLFLQSKSKHLLTNEFPDPTGKTCCLKAMINLHDGQNTT 173
QY 210 IPLLDAERTGNMREFFINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 269
DB 174 IPLLDAERTGNMREFFINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 233
QY 270 GREFQPDGEGYFPGELPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 329
DB 234 GDEFFKTKGRPGFYFGLPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 293
QY 330 AIDNRENTKFTYKMYDLILKCARLPDSNLEAVINNDGLSPIMAAATGKIGIHOI 389
DB 294 EVADNTADNTKFTYKMYDLILKCARLPDSNLEAVINNDGLSPIMAAATGKIGIHOI 353
QY 390 IREVTDEDTRLSRKPKDWAYGVYSSLYDLSLDTGCEASVLEIIVY-NSKIERRHE 448
DB 354 LOREIOPEBCRHLSRKFTEWAYGVHSLYDLSLDTGCEASVLEIIVY-NSKIERRHE 412
QY 449 MAVEPINELLRKMRKFGAVSFYINVSYLCAVITFTLTAAYOPLGTPPYRYRTVDY 508
DB 413 MLVEPINELLRKMRKFGAVSFYINVSYLCAVITFTLTAAYOPLGTPPYRYRTVDY 472
QY 509 LRLAGEVITLFTGVLFPEFTNIDLFMKKCPGVNSLFDISGFLLYFYSVLVISAALYL 568
DB 473 FRTYGBLSLVGVSFFFRIGIQ-YFLORBSMKTLFVDSSEMLFLOSIFMLATVLYLF 531
QY 569 AGIEAVLAVWVFLVGMNVALYTRGLKLTGYTSIMIQKLEKDFRPLVLYLLFMIGY 628
DB 532 SHKEVYAVWVFLVGMNVALYTRGLKLTGYTSIMIQKLEKDFRPLVLYLLFMIGY 591
QY 629 ASALVSLNPCANMKVCNEDQNCVPTY-----PSCRDET-----FSTFLDLFK 675
DB 592 STAVVTLI-----EDGKNDSLPSESTSHRWGAPACRPDSSVNSLYST-CLELFX 640
QY 676 LITGMGDLMLSTKPYVFIILVYIITFVLLNMLIALMGFTVGVGSKESKRIWKL 735
DB 641 FTIGMDLEFTEYDFAVFIILVYIITFVLLNMLIALMGFTVGVGSKESKRIWKL 700
QY 736 Q 736
DB 701 Q 701

RESULT 15
US-09-197-636-4
; Sequence 4, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID
; APPLICANT: HAYES, PHILIP
; APPLICANT: MEADOWS, HELEN
; APPLICANT: DAVIS, JOHN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; STREET: P. O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:

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1 CEDIUM TYPE: IBM Compatible
2 COMPUTER: IBM Compatible
3 OPERATING SYSTEM: DOS
4 SOFTWARE: FASTSEQ for Windows Vert
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/09/197, 636
7 FILING DATE: 23-NOV-1998
8 CLASSIFICATION:
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: UK 9805137.8
11 FILING DATE: 12-MAR-1998
12 APPLICATION NUMBER: UK 9815791.0
13 FILING DATE: 21-JUL-1998
14 APPLICATION NUMBER: UK 9819278.4
15 FILING DATE: 03-SEP-1998
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Prestia, Paul P
18 REGISTRATION NUMBER: 23, 031
19 REFERENCE/DOCKET NUMBER: GP-30075
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 601-407-0700
22 TELEFAX: 610-407-0701
23 TELEX: 946169
24 INFORMATION FOR SEQ ID NO: 4:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 839 amino acids
27 TYPE: amino acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: protein
31
32 US-09/197-636-4

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Query Match	40.2%;	Score 1552.5;	DB 3;	Length 839;
Best Local Similarity	44.4%;	Pred. No. 1.1e-138;		
Matches 320;	Conservative 189;	Mismatches 189;	Indels 74;	Gaps 12

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0Y      49 FSPADASRPAGDGKREML-----RMKQG-----ARKGPNIDLES--TLYESSV 95
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      22 PDLPLGDGNRSRPPAKPOLSTAKSRTLRFGKDSSEAFVDCPHBEGELSDCPTTLFV 81
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      96 V-----POPKAPMDSLFDGYTVRHHSNDNKRMRKKTIEKOPSGPKAPOPPIIKVF 149
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      82 ITTORPGDCEFTARL-----LQDSVAASTEXTRLRY 113
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      150 NEPIIFDIYSRGSTADLDGLPELLTHKKRLTDEEFREPSTGTCLPKALINLSGRND 209
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      114 DRSRIFEANAQNOCODLESLILFLQSKKGXVDNEKPDBETGTCILKAMLIHGOQNTT 173
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      210 IPVLIDIAERTGMMEPFINSPPRDYYRGOTAHIAIERCKHYELLVAQADVAQAOR 269
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      174 IPLLLEIAFOQTSLKELVNAXYTDXXYKQOTAHIAIERNNALVTLLVENAGDVQAAN 233
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      270 GRFPQKOBGVFYFGEPLPLSLACTNOGHIVNYLTENEPHKADMRQDSRGTVLHALV 329
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      234 GPFPKTKGRPGFYGEPLPLSLACTNOIGIYKFLQNSWQRDAIRBSVGNTVLHALV 293
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      330 AIADNTRNTKFYKYAYDLLLKCARLPEDSNILEAVLNNDGLSPIMAAKTKGIIFOHI 389
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      294 EVADNADNMTKFTVMYNELLIGAKLHPTELKLEITNNKMTPMALAAGTGCTGLAYI 353
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      390 IRREVTDERTRIHSRKFKDMAYGPVYSSLYDLSLDTQCBEASVAILVY-NKIENRBH 448
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      354 LQREIOBPCCRHRISRFTEMAVPVHSSLYDLSIDTC-EKNSVLVIVAASSETNRHD 412
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      449 M'AVEP'INELBRMKMKFGAVSYFINWSYLCAVIFTLTAAYQDPLEGTPPYRYRTLVY 508
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      413 ML'AVEP'INLLODKMDRFVKRIITYFNFPLYCLMIIFTMAARYRRPDGLPRFMKXTG DY 472
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      509 LR'LAGEVITLFTSVLFETFNIKOLFEMKKCGVNSLFDIGSFOLLTYTFYVSVAIALYL 568
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      473 FYATGSILSLVGSVYFFPGIO-YFLQBRBSMTKLTFVDSYSEMILFPOSLEMLATVLYE 531
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      569 AGIEAVLAVMPALVIGMMNALYFTGKLITGYYSIMICKLIEFKDLERILLVYLLPMIGY 628

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[illegible]

Search completed: December 2, 2004, 22:36:13
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2004, 22:26:51 ; Search time 148 Seconds

(without alignments)
1787.935 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSSGPRAGPGEVAFLEP.....GVYSKSKHIMWLQSGRRRL 742

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	14	US-10-090-215-12
2	3829	99.2	831	15	US-10-342-844-76
3	3829	99.2	870	16	US-10-761-065-2
4	3829	99.2	871	10	US-09-870-090-2
5	3829	99.2	871	14	US-10-000-823-7
6	3829	99.2	871	14	US-10-171-319-7
7	3829	99.2	871	15	US-10-342-844-54
8	3829	99.2	871	15	US-10-342-844-58
9	3829	99.2	871	15	US-10-342-844-78
10	3829	99.2	871	17	US-10-415-570A-2
11	3828	99.2	871	14	US-10-027-828-2
12	3828	99.2	871	15	US-10-342-844-60
13	3825	99.1	871	14	US-10-027-828-4

14	3823	99.1	871	14	US-10-090-215-7	Sequence 7, Appli
15	3810	98.8	963	10	US-09-932-165-1477	Sequence 1477, Ap
16	3809	98.7	871	14	US-10-227-255A-3	Sequence 3, Appli
17	3695	95.8	871	15	US-10-342-844-84	Sequence 84, Appli
18	3693	95.7	830	14	US-10-027-828-6	Sequence 6, Appli
19	3693	95.7	871	14	US-10-027-828-11	Sequence 11, Appli
20	3693	95.7	871	15	US-10-342-844-66	Sequence 66, Appli
21	3689	95.6	871	15	US-10-342-844-80	Sequence 80, Appli
22	3687	95.6	871	14	US-10-027-828-10	Sequence 10, Appli
23	3686	95.5	871	14	US-10-027-828-8	Sequence 8, Appli
24	3686	95.5	871	14	US-10-027-828-9	Sequence 9, Appli
25	3685	95.5	871	14	US-10-171-319-14	Sequence 14, Appli
26	3681	95.4	871	14	US-10-227-255A-1	Sequence 1, Appli
27	3652	94.7	870	14	US-10-027-828-13	Sequence 13, Appli
28	3636	94.2	873	15	US-10-342-844-64	Sequence 64, Appli
29	3472	90.0	803	15	US-10-342-844-56	Sequence 56, Appli
30	3470	89.9	811	14	US-10-090-215-9	Sequence 9, Appli
31	3467	89.9	792	9	US-09-764-367A-2	Sequence 2, Appli
32	3457	89.6	803	9	US-09-764-367A-8	Sequence 8, Appli
33	3389	87.8	803	15	US-10-342-844-62	Sequence 62, Appli
34	3284	85.1	852	14	US-10-027-828-15	Sequence 15, Appli
35	3284	85.1	852	15	US-10-342-844-36	Sequence 36, Appli
36	3120	80.9	743	9	US-09-764-367A-11	Sequence 11, Appli
37	3044.5	78.9	734	9	US-09-764-367A-4	Sequence 4, Appli
38	2847	73.8	625	10	US-09-932-165-1507	Sequence 1507, Ap
39	2782	72.1	625	10	US-09-932-165-1506	Sequence 1506, Ap
40	2373.5	61.5	602	10	US-09-870-090-4	Sequence 4, Appli
41	2373.5	61.5	602	16	US-10-761-065-4	Sequence 4, Appli
42	2156.5	55.9	559	14	US-10-297-022-10	Sequence 10, Appli
43	1808	46.9	498	14	US-10-168-651-2	Sequence 2, Appli
44	1622	42.0	420	14	US-10-027-828-7	Sequence 7, Appli
45	1622	42.0	461	14	US-10-027-828-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-090-215-12
; Sequence 12, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glaes, Charles A
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/090,215
; CURRENT FILING DATE: 2002-03-04
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-215-12

Query Match 100.0%; Score 3858; DB 14; Length 742;
Best Local Similarity 100.0%; Pred. No. 1.7e-307;
Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSSGPRAGPGEVAFLEPDSGTPGGEAPPLSLANIFEGEDSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAFLEPDSGTPGGEAPPLSLANIFEGEDSLSPSPADASRPAGP 60
QY 61 GDGPNILMKFGAFKFKVNPIDLESTLYESSVVPKPKAPMDSLDYGYRHSSDN 120
DB 61 GDGPNILMKFGAFKFKVNPIDLESTLYESSVVPKPKAPMDSLDYGYRHSSDN 120
QY 121 KRMKKITEKQPSGPKADAPQPPILKVFNPILFDIVSRGSTADLDGLPFLTHKKRL 180
DB 121 KRMKKITEKQPSGPKADAPQPPILKVFNPILFDIVSRGSTADLDGLPFLTHKKRL 180

D	b	121	KRMKKKIIENKQSPGPKAPAPQEPPIIKVFNPNPIEFDIVSRGSTALDGLPELTHKKSL	180
Q	y	181	TDESEFREPSTGKTCLPKALMLNSGRNDTTPYLLDIARTGMRREFINSFPFDIYYRGOT	240
D	b	181	TDEEFREBSTGKTCLPKALMLNSGRNDTTPYLLDIARTGMRREFINSFPFDIYYRGOT	240
Q	y	241	ALHAIATERCHAYEELLVAOGADVHAOARGFPOKDEGGYFPGHLPJSLAACTNOPIH	300
D	b	241	ALHAIATERCHAYEELLVAOGADVHAOARGFPOKDEGGYFPGHLPJSLAACTNOPIH	300
Q	y	301	VNYLTLENHKKADMRQDSRGNTVLAHALVALADNTRENTKPYTKMYDLILKCARLPDS	360
D	b	301	VNYLTLENHKKADMRQDSRGNTVLAHALVALADNTRENTKPYTKMYDLILKCARLPDS	360
Q	y	361	NLEAVLNNDGJSPILMAAKTGKIGIFOHIIREAVTDEDPRHLSRKPKDMAYGVSYSLD	420
D	b	361	NLEAVLNNDGJSPILMAAKTGKIGIFOHIIREAVTDEDPRHLSRKPKDMAYGVSYSLD	420
Q	y	421	LSLSDTCGEBAVSYLEILVYNSKIENRHEMLAVEPINELLRDXMRKGAVSPYINVSYSIC	480
D	b	421	LSLSDTCGEBAVSYLEILVYNSKIENRHEMLAVEPINELLRDXMRKGAVSPYINVSYSIC	480
Q	y	481	AMVIFTLTAYOPLBEGTPPYPRRTTYDYRLAGEVYTLTGVLFFFTINIKDLEPMKCPQV	540
D	b	481	AMVIFTLTAYOPLBEGTPPYPRRTTYDYRLAGEVYTLTGVLFFFTINIKDLEPMKCPQV	540
Q	y	541	NSLFFDGSFOLLIFYYSVYVIVSAAIYLAGIEAYLAVMFAVLGMMNNAIFYRGKLTG	600
D	b	541	NSLFFDGSFOLLIFYYSVYVIVSAAIYLAGIERIYLAVMFAVLGMMNNAIFYRGKLTG	600
Q	y	601	TYSIMIOKILFNDREFLLVYLLFMIGYASALVSLNPPCANMKVCNEDQNTCTVPTPSPC	660
D	b	601	TYSIMIOKILFNDREFLLVYLLFMIGYASALVSLNPPCANMKVCNEDQNTCTVPTPSPC	660
Q	y	661	RDSEFFSTFLDLFKLTTIGMDLEMLSSRKYPVVFIIILVTVYIILFVYLLINMLALMGE	720
D	b	661	RDSEFFSTFLDLFKLTTIGMDLEMLSSRKYPVVFIIILVTVYIILFVYLLINMLALMGE	720
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D	b	721	TVGQVSKESKHIMKLOSGRRL 742	

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RESULT 2
US-10-342-844-76
/ Sequence 76, Application US/10342844
/ Publication No. US20040009537A1
/ GENERAL INFORMATION:
/ APPLICANT: Roos, Jack
/ APPLICANT: Stauderman, Kenneth
/ APPLICANT: Velicelbi, G'n.1
/ TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
/ TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
/ FILE REFERENCE: 37481-3307
/ CURRENT APPLICATION NUMBER: US/10/342,844
/ CURRENT FILING DATE: 2003-01-13
/ PRIOR APPLICATION NUMBER: US 60/347,459
/ PRIOR FILING DATE: 2002-01-11
/ PRIOR APPLICATION NUMBER: US 60/401,171
/ PRIOR FILING DATE: 2002-08-02
/ PRIOR APPLICATION NUMBER: US 60/405,678
/ PRIOR FILING DATE: 2002-08-20
/ NUMBER OF SEQ ID NOS: 115
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 76
/ LENGTH: 831
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: 804, 816
/ OTHER INFORMATION: Xaa = Any Amino Acid
/ PUBLICATION INFORMATION:
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; DATABASE ACCESSION NUMBER: Genbank XP_012261
; DATABASE ENTRY DATE: 2001-10-16
US-10-342-844-76

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Query Match	99.2%	Score 3829	DB 15	Length 831
Best Local Similarity	100.0%	Pred. No. 5e-305		
Matches 736	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Db	1	MADSSBGRAPGVEVAELPGBSSGIPQGEAPLPSLSLALFJGBDSSLSPSPADASRPAGP	60
Qy	61	GDGRPNLMMKQGAFRKVPNPIDLBESTLYESSVSPCKKAPMOSLDDYGYRRHSSDN	120
Db	61	GDGRPNLMMKQGAFRKVPNPIDLBESTLYESSVSPCKAPMOSLDDYGYRRHSSDN	120
Qy	121	KWRKKIIEKQPOSKAPAPOPPLIKFVNRPIIFDIYSRGSATDIDLPLPLTHKKRL	180
Db	121	KWRKKIIEKQPOSKAPAPOPPLIKFVNRPIIFDIYSRGSATDIDLPLPLTHKKRL	180
Qy	181	TDEBFRBPSGTGTCPLKALINLSNGRNTIIPVLLDIAERTGMREPIINSPPPDIIYRGOT	240
Db	181	TDEBFRBPSGTGTCPLKALINLSNGRNTIIPVLLDIAERTGMREPIINSPPPDIIYRGOT	240
Qy	241	ALHIAIERCKHYVELLYAOGADVAOAKRGAPFOPKDBGGYTYFPELPISLAACNPOHI	300
Db	241	ALHIAIERCKHYVELLYAOGADVAOAKRGAPFOPKDBGGYTYFPELPISLAACNPOHI	300
Qy	301	VNYVLTENHHKKADMRODSRGNTVHALVALADNTRRENTKPYTKAWDLILKCARLFPS	360
Db	301	VNYVLTENHHKKADMRODSRGNTVHALVALADNTRRENTKPYTKADILLKCARLFPS	360
Qy	361	NLEAVLNDGSLPSLMAAAKTGKIGIFOHIIIRREVTDIEDTRHLSRKFKMAVAPVYSSLYD	420
Db	361	NLEAVLNDGSLPSLMAAAKTGKIGIFOHIIIRREVTDIEDTRHLSRKFKMAVAGVYSSLYD	420
Qy	421	ISSLDTCGEASVELLYVNSKIENRHEMLAVEPINELLRDQWRKGAVSFYINNVSYIC	480
Db	421	ISSLDTCGEASVELLYVNSKIENRHEMLAVEPINELLRDQWRKGAVSFYINNVSYIC	480
Qy	481	ANVIFLTLTAAYQPLBETSPYPRTTVDYRLAGEVITLFTGVLFPEFTNIKDLFMKKCPGV	540
Db	481	ANVIFLTLTAAYQPLBETSPYPRTTVDYRLAGEVITLFTGVLFPEFTNIKDLFMKKCPGV	540
Qy	541	NSLFIIDGSPQLLYFYISVLYISAAIYLAGIEAYLAVMFAVLGMNMLFYTRGLKLTG	600
Db	541	NSLFIIDGSPQLLYFYISVLYISAAIYLAGIEAYLAVMFAVLGMNMLFYTRGLKLTG	600
Qy	601	TVYSIMIOKILFKDLFRFELLVYLLPMIYGASALVSLNPPCANMVCNEDQNTCVPIYPSC	660
Db	601	TVYSIMIOKILFKDLFRFELLVYLLPMIYGASALVSLNPPCANMVCNEDQNTCVPIYPSC	660
Qy	661	ROSEFTSTLLDLFKLITMGDLEMSTRKYPVFIIILVYTIILFVLLINMLIALMGE	720
Db	661	ROSEFTSTLLDLFKLITMGDLEMSTRKYPVFIIILVYTIILFVLLINMLIALMGE	720
Qy	721	TVGQVSKESHKIWLQ 736	
Db	721	TVGQVSKESHKIWLQ 736	

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RESULT 3
US-10-761-065-2
; Sequence 2, Application US/10761065
; Publication No. US20040137573A1
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; GENERAL INFORMATION:
;
; APPLICANT: Pfizer, Inc.
; APPLICANT: Katsuhito Shinjo
; APPLICANT: Hiikaru Yabuchi
; TITLE OF INVENTION: Human Vanilloid Receptor-like Proteins
; FILE REFERENCE: PC99796ADAM
; CURRENT APPLICATION NUMBER: US/10/761, 065
; CURRENT FILING DATE: 2004-01-20
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; PRIOR APPLICATION NUMBER: US/09/870,090A
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: US 60/208,156
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 870
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-10-761-065-2

Query Match 99.2%; Score 3829; DB 16; Length 870;
 Best Local Similarity 100.0%; Pred. No. 5.3e-305;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADSSGPRAGPEVEALPGDESGTGGGAFFPLSLANFEGDGLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPEVEALPGDESGTGGGAFFPLSLANFEGDGLSPSPADASRPAGP 60
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DB 61 GGRPMLRMKFGAFAKGVNPIDLESTLYESSVPGPKAPMDSLFDYGYRHSSDN 120
QY 121 KWRKKIIEKQPSKAPAPQPPILKVNRPILFDIVSRGTADLDGLPLLTTHKKL 180
DB 121 KWRKKIIEKQPSKAPAPQPPILKVNRPILFDIVSRGTADLDGLPLLTTHKKL 180
QY 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPVLDAERTGNMREINSPFRDIYRGQT 240
DB 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPVLDAERTGNMREINSPFRDIYRGQT 240
QY 241 ALHAIERRCKHYVELVAQADVAQAARGFPQPDGEGYFEGELPLSLAATNQPHI 300
DB 241 ALHAIERRCKHYVELVAQADVAQAARGFPQPDGEGYFEGELPLSLAATNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKWDLLILLCARLFPS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKWDLLILLCARLFPS 360
QY 361 NLEAVLNDGSLPLMAAKTGKIGI FOHIIRREVDDETRHLSRKFQMAAGPVYSSLYD 420
DB 361 NLEAVLNDGSLPLMAAKTGKIGI FOHIIRREVDDETRHLSRKFQMAAGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
QY 481 AMVITTLTAAYQPLGTPPYRTTVDYRLAGEVITLFTGVLPFTNIKDLFMKCPGV 540
DB 481 AMVITTLTAAYQPLGTPPYRTTVDYRLAGEVITLFTGVLPFTNIKDLFMKCPGV 540
QY 541 NSLFDGSGFOLLFFYSVLVIVSALYLAGIAYAVWVFAVLGMMNALVYTRGKLGTG 600
DB 541 NSLFDGSGFOLLFFYSVLVIVSALYLAGIAYAVWVFAVLGMMNALVYTRGKLGTG 600
QY 601 TYSIMIQKILFKDLRFLVYLLEMIGYASALVSLNFCAMNKVCNEQNTCTVPTYPSC 660
DB 601 TYSIMIQKILFKDLRFLVYLLEMIGYASALVSLNFCAMNKVCNEQNTCTVPTYPSC 660
QY 661 RDSEFTFTLLDLFKLITGMGDEMLSTKYPVVFIIILVYIIITFVILLNMLTALMGE 720
DB 661 RDSEFTFTLLDLFKLITGMGDEMLSTKYPVVFIIILVYIIITFVILLNMLTALMGE 720
QY 721 TVGVSKSKSHIWKLO 736
DB 721 TVGVSKSKSHIWKLO 736

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RESULT 4
 US-09-870-090-2
 ; Sequence 2, Application US/09870090
 ; Publication No. US20030017527A1

; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Product Inc.
 ; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins
 ; FILE REFERENCE: PC9979A
 ; CURRENT APPLICATION NUMBER: US/09/870,090
 ; CURRENT FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: US 60/208,156
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-870-090-2

Query Match 99.2%; Score 3829; DB 10; Length 871;
 Best Local Similarity 100.0%; Pred. No. 5.3e-305;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MADSSGPRAGPEVEALPGDESGTGGGAFFPLSLANFEGDGLSPSPADASRPAGP 60
QY 61 GGRPMLRMKFGAFAKGVNPIDLESTLYESSVPGPKAPMDSLFDYGYRHSSDN 120
DB 61 GGRPMLRMKFGAFAKGVNPIDLESTLYESSVPGPKAPMDSLFDYGYRHSSDN 120
QY 121 KWRKKIIEKQPSKAPAPQPPILKVNRPILFDIVSRGTADLDGLPLLTTHKKL 180
DB 121 KWRKKIIEKQPSKAPAPQPPILKVNRPILFDIVSRGTADLDGLPLLTTHKKL 180
QY 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPVLDAERTGNMREINSPFRDIYRGQT 240
DB 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPVLDAERTGNMREINSPFRDIYRGQT 240
QY 241 ALHAIERRCKHYVELVAQADVAQAARGFPQPDGEGYFEGELPLSLAATNQPHI 300
DB 241 ALHAIERRCKHYVELVAQADVAQAARGFPQPDGEGYFEGELPLSLAATNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKWDLLILLCARLFPS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKWDLLILLCARLFPS 360
QY 361 NLEAVLNDGSLPLMAAKTGKIGI FOHIIRREVDDETRHLSRKFQMAAGPVYSSLYD 420
DB 361 NLEAVLNDGSLPLMAAKTGKIGI FOHIIRREVDDETRHLSRKFQMAAGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
QY 481 AMVITTLTAAYQPLGTPPYRTTVDYRLAGEVITLFTGVLPFTNIKDLFMKCPGV 540
DB 481 AMVITTLTAAYQPLGTPPYRTTVDYRLAGEVITLFTGVLPFTNIKDLFMKCPGV 540
QY 541 NSLFDGSGFOLLFFYSVLVIVSALYLAGIAYAVWVFAVLGMMNALVYTRGKLGTG 600
DB 541 NSLFDGSGFOLLFFYSVLVIVSALYLAGIAYAVWVFAVLGMMNALVYTRGKLGTG 600
QY 601 TYSIMIQKILFKDLRFLVYLLEMIGYASALVSLNFCAMNKVCNEQNTCTVPTYPSC 660
DB 601 TYSIMIQKILFKDLRFLVYLLEMIGYASALVSLNFCAMNKVCNEQNTCTVPTYPSC 660
QY 661 RDSEFTFTLLDLFKLITGMGDEMLSTKYPVVFIIILVYIIITFVILLNMLTALMGE 720
DB 661 RDSEFTFTLLDLFKLITGMGDEMLSTKYPVVFIIILVYIIITFVILLNMLTALMGE 720
QY 721 TVGVSKSKSHIWKLO 736
DB 721 TVGVSKSKSHIWKLO 736

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QY 421 LSLDTCGEASVLEILLVNSKIENRHEMLAVEPINELLDRKRRKGAVSFYINVSYLK 480
DB 421 LSLDTCGEASVLEILLVNSKIENRHEMLAVEPINELLDRKRRKGAVSFYINVSYLK 480
QY 481 AMVIFLTLAYYQPLBGTPEPYRTTYDYLRLAGEVITLFTGVLFETTNIKDLFMKKCPGV 540
DB 481 AMVIFLTLAYYQPLBGTPEPYRTTYDYLRLAGEVITLFTGVLFETTNIKDLFMKKCPGV 540
QY 541 NSLFDGSPQLLYFYISVLYVSALVYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFYISVLYVSALVYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
QY 601 TYSIMOKTLPKDLFPFLVYLLFMIGVASALVSLINPCANMKVCNEDQNTCTVPTYPSC 660
DB 601 TYSIMOKTLPKDLFPFLVYLLFMIGVASALVSLINPCANMKVCNEDQNTCTVPTYPSC 660
QY 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVVFVILLVYIILLFVLLINMLIALMGE 720
DB 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVVFVILLVYIILLFVLLINMLIALMGE 720
QY 721 TVGVSKSKSHIMKLO 736
DB 721 TVGVSKSKSHIMKLO 736

RESULT 7

US-10-342-844-54
; Sequence 54, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Staudeman, Kenneth
; APPLICANT: Velicelebi, G'n 1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342, 844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347, 459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401, 171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405, 678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 871
; TYPE: prt
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank XP_027181
; DATABASE ENTRY DATE: 2002-09-01
US-10-342-844-54

Query Match 99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 5.3e-305;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGAYVLELPGDESGTPGGAFLPSLIANLFEEDGSLSPADASRPAP 60
DB 1 MADSEGPAGGAYVLELPGDESGTPGGAFLPSLIANLFEEDGSLSPADASRPAP 60
QY 61 GGGRENLMKFGAARKGVPNPIDLESTLYESSVVPKKAAMDLSFDYGYRRHSSN 120
DB 61 GGGRENLMKFGAARKGVPNPIDLESTLYESSVVPKKAAMDLSFDYGYRRHSSN 120
QY 121 KMKRKIIIEKQPSKAPAPPPPIIKVFNRPILFDIVSRGSTADLDGLLPLTHKKKL 180
DB 121 KMKRKIIIEKQPSKAPAPPPPIIKVFNRPILFDIVSRGSTADLDGLLPLTHKKKL 180
QY 181 TDEEFPSTGTCTPKALNLSNGRNDIIPVLLIABRTGMRERINPPFDIYYRGOT 240
DB 181 TDEEFPSTGTCTPKALNLSNGRNDIIPVLLIABRTGMRERINPPFDIYYRGOT 240

DB 181 TDEEFPSTGTCTPKALNLSNGRNDIIPVLLIABRTGMRERINPPFDIYYRGOT 240
QY 241 ALHIAIERCKKHVELLVNOGADVHOAGRFQPPDEGXYFFPGLPLSLACTOPHI 300
DB 241 ALHIAIERCKKHVELLVNOGADVHOAGRFQPPDEGXYFFPGLPLSLACTOPHI 300
QY 301 VNYLTENPKKADMRQDSRGNTVLAVALADNTRNTKVFYKMDLILKCARLPDS 360
DB 301 VNYLTENPKKADMRQDSRGNTVLAVALADNTRNTKVFYKMDLILKCARLPDS 360
QY 361 NIEAVLNNDGSLPMAAATKIGIFQHIIRREVTEDTRHLSRKKEDMAVYGSLLYD 420
DB 361 NIEAVLNNDGSLPMAAATKIGIFQHIIRREVTEDTRHLSRKKEDMAVYGSLLYD 420
QY 421 LSLDTCGEASVLEILLVNSKIENRHEMLAVEPINELLDRKRRKGAVSFYINVSYLK 480
DB 421 LSLDTCGEASVLEILLVNSKIENRHEMLAVEPINELLDRKRRKGAVSFYINVSYLK 480
QY 481 AMVIFLTLAYYQPLBGTPEPYRTTYDYLRLAGEVITLFTGVLFETTNIKDLFMKKCPGV 540
DB 481 AMVIFLTLAYYQPLBGTPEPYRTTYDYLRLAGEVITLFTGVLFETTNIKDLFMKKCPGV 540
QY 541 NSLFDGSPQLLYFYISVLYVSALVYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFYISVLYVSALVYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
QY 601 TYSIMOKTLPKDLFPFLVYLLFMIGVASALVSLINPCANMKVCNEDQNTCTVPTYPSC 660
DB 601 TYSIMOKTLPKDLFPFLVYLLFMIGVASALVSLINPCANMKVCNEDQNTCTVPTYPSC 660
QY 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVVFVILLVYIILLFVLLINMLIALMGE 720
DB 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVVFVILLVYIILLFVLLINMLIALMGE 720
QY 721 TVGVSKSKSHIMKLO 736
DB 721 TVGVSKSKSHIMKLO 736

RESULT 8

US-10-342-844-58
; Sequence 58, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Staudeman, Kenneth
; APPLICANT: Velicelebi, G'n 1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342, 844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347, 459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401, 171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405, 678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 871
; TYPE: prt
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank BAB69040
; DATABASE ENTRY DATE: 2001-10-02
US-10-342-844-58

Query Match 99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 5.3e-305;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPEVAELPDDESSTPGGEAFPLSSIANLFEGBDGSISPSPADASRAGP 60
DB 1 MADSSGPRAGPEVAELPDDESSTPGGEAFPLSSIANLFEGBDGSISPSPADASRAGP 60
QY 61 GDERPMLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAMDSLFDTYRRHSSDN 120
DB 61 GDERPMLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAMDSLFDTYRRHSSDN 120
QY 121 KMRKKTIEKOPSPKAPAPQPPILKVENRPIILFDVSRGSTADLDGLPFLTHKKRL 180
DB 121 KMRKKTIEKOPSPKAPAPQPPILKVENRPIILFDVSRGSTADLDGLPFLTHKKRL 180
QY 181 TDEEFREPSGTCTCLPKALNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYYRGQT 240
DB 181 TDEEFREPSGTCTCLPKALNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYYRGQT 240
QY 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPKDEGGYFFGELPLSLACTIONS 300
DB 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPKDEGGYFFGELPLSLACTIONS 300
QY 301 VNYLTENPHKADMRRODSRGNTVLAHVAIADNTRENTKFTVMYDLILKCARLPDS 360
DB 301 VNYLTENPHKADMRRODSRGNTVLAHVAIADNTRENTKFTVMYDLILKCARLPDS 360
QY 361 NLEAVLNNDGLSPIMMAKTGKIGIFQHIIRREVTDEDTLHLSKRFOMAYGVPYSSLYD 420
DB 361 NLEAVLNNDGLSPIMMAKTGKIGIFQHIIRREVTDEDTLHLSKRFOMAYGVPYSSLYD 420
QY 421 LSSLDTCGEASVIELIVNSKIENRHEMLAVEINLBDKMKKFAVSFIYINVSYL 480
DB 421 LSSLDTCGEASVIELIVNSKIENRHEMLAVEINLBDKMKKFAVSFIYINVSYL 480
QY 481 AMYIFLTAAYQPLEGTPPYPRRTVDYLRAGEVITLFTGVLEFFTNIDLFMKKCPGV 540
DB 481 AMYIFLTAAYQPLEGTPPYPRRTVDYLRAGEVITLFTGVLEFFTNIDLFMKKCPGV 540
QY 541 NSLFIDGSFOLLVFIYSVLIVSALYLAGIEALVAVPALVIGMNAALYFTGKL 600
DB 541 NSLFIDGSFOLLVFIYSVLIVSALYLAGIEALVAVPALVIGMNAALYFTGKL 600
QY 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLPCANMKYCNDQNTCTVPTPSC 660
DB 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLPCANMKYCNDQNTCTVPTPSC 660
QY 661 RDSSTFTFLDLFKLTIGMDLEMLSTKXPVVFIIILVYIILTFVLLNMLIALMGE 720
DB 661 RDSSTFTFLDLFKLTIGMDLEMLSTKXPVVFIIILVYIILTFVLLNMLIALMGE 720
QY 721 TVGQVSRESKHIWKLQ 736
DB 721 TVGQVSRESKHIWKLQ 736

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 871
; TYPE: PR
; ORGANISM: Homo sapiens
; PUBLICATON INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAG16127
; DATABASE ENTRY DATE: 2000-09-26
; US-10-342-844-78

Query Match      99.2%  Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 5.3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAGPEVAELPDDESSTPGGEAFPLSSIANLFEGBDGSISPSPADASRAGP 60
DB 1 MADSSGPRAGPEVAELPDDESSTPGGEAFPLSSIANLFEGBDGSISPSPADASRAGP 60
QY 61 GDERPMLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAMDSLFDTYRRHSSDN 120
DB 61 GDERPMLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAMDSLFDTYRRHSSDN 120
QY 121 KMRKKTIEKOPSPKAPAPQPPILKVENRPIILFDVSRGSTADLDGLPFLTHKKRL 180
DB 121 KMRKKTIEKOPSPKAPAPQPPILKVENRPIILFDVSRGSTADLDGLPFLTHKKRL 180
QY 181 TDEEFREPSGTCTCLPKALNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYYRGQT 240
DB 181 TDEEFREPSGTCTCLPKALNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYYRGQT 240
QY 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPKDEGGYFFGELPLSLACTIONS 300
DB 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPKDEGGYFFGELPLSLACTIONS 300
QY 301 VNYLTENPHKADMRRODSRGNTVLAHVAIADNTRENTKFTVMYDLILKCARLPDS 360
DB 301 VNYLTENPHKADMRRODSRGNTVLAHVAIADNTRENTKFTVMYDLILKCARLPDS 360
QY 361 NLEAVLNNDGLSPIMMAKTGKIGIFQHIIRREVTDEDTLHLSKRFOMAYGVPYSSLYD 420
DB 361 NLEAVLNNDGLSPIMMAKTGKIGIFQHIIRREVTDEDTLHLSKRFOMAYGVPYSSLYD 420
QY 421 LSSLDTCGEASVIELIVNSKIENRHEMLAVEINLBDKMKKFAVSFIYINVSYL 480
DB 421 LSSLDTCGEASVIELIVNSKIENRHEMLAVEINLBDKMKKFAVSFIYINVSYL 480
QY 481 AMYIFLTAAYQPLEGTPPYPRRTVDYLRAGEVITLFTGVLEFFTNIDLFMKKCPGV 540
DB 481 AMYIFLTAAYQPLEGTPPYPRRTVDYLRAGEVITLFTGVLEFFTNIDLFMKKCPGV 540
QY 541 NSLFIDGSFOLLVFIYSVLIVSALYLAGIEALVAVPALVIGMNAALYFTGKL 600
DB 541 NSLFIDGSFOLLVFIYSVLIVSALYLAGIEALVAVPALVIGMNAALYFTGKL 600
QY 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLPCANMKYCNDQNTCTVPTPSC 660
DB 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLPCANMKYCNDQNTCTVPTPSC 660
QY 661 RDSSTFTFLDLFKLTIGMDLEMLSTKXPVVFIIILVYIILTFVLLNMLIALMGE 720
DB 661 RDSSTFTFLDLFKLTIGMDLEMLSTKXPVVFIIILVYIILTFVLLNMLIALMGE 720
QY 721 TVGQVSRESKHIWKLQ 736
DB 721 TVGQVSRESKHIWKLQ 736

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RESULT 9
US-10-342-844-78
; Sequence 78, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Velicelbi, G'n_1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115

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RESULT 10
US-10-415-570A-2
; Sequence 2, Application US/10415570A
; Publication No. US20040198649A1
; GENERAL INFORMATION:
; APPLICANT: Davis, John Beresford

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; APPLICANT: Gunthorpe, Martin James
; APPLICANT: Egerton, Julie
; APPLICANT: Smart, Darren
; TITLE OF INVENTION: New Use
; FILE REFERENCE: P32689
; CURRENT APPLICATION NUMBER: US/10/415,570A
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/GB01/04739
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: GB 0026114.9
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-415-570A-2

```

```

Query Match          99.2%; Score 3829; DB 17; Length 871;
Best Local Similarity 100.0%; Pred. No. 5.3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MADSSGPRAGPGEVAELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60
D 1 MADSSGPRAGPGEVAELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60
QY 61 GDRPMLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAMDSLFDYGYRHHSSDN 120
D 61 GDRPMLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAMDSLFDYGYRHHSSDN 120
QY 121 KWRKKIIEKOPSPAPAPQPPILKVENRPLIFDIVSGSTADLDGLPFLTHKKRL 180
D 121 KWRKKIIEKOPSPAPAPQPPILKVENRPLIFDIVSGSTADLDGLPFLTHKKRL 180
QY 181 TDEEFEPSTGTCCLPKALINSNGNDITPVLDIAERTGNRREFINSFPRDIYRGOT 240
D 181 TDEEFEPSTGTCCLPKALINSNGNDITPVLDIAERTGNRREFINSFPRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYGELPLSLAQTNPPI 300
D 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYGELPLSLAQTNPPI 300
QY 301 VVLTENPKKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDILLKCARLFPDS 360
D 301 VVLTENPKKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDILLKCARLFPDS 360
QY 361 NLEAVANNQGLSPLMMAATGKIGIPOHIIIRREVTDEDRHLSRKFKDWAYGVSISLD 420
D 361 NLEAVANNQGLSPLMMAATGKIGIPOHIIIRREVTDEDRHLSRKFKDWAYGVSISLD 420
QY 421 LSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDKWRKGAVSFYINVSYL 480
D 421 LSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDKWRKGAVSFYINVSYL 480
QY 481 AVVIFLTAAYQPLEBGTPPYPRRTVDYRLAGEVITLFTGVLFPTNKKDLFMKCPGV 540
D 481 AVVIFLTAAYQPLEBGTPPYPRRTVDYRLAGEVITLFTGVLFPTNKKDLFMKCPGV 540
QY 541 NSLFDGSPQLLYFYISVIVISAALYLAGIEAYLAWMFALVGMNMLYFTRGKLTG 600
D 541 NSLFDGSPQLLYFYISVIVISAALYLAGIEAYLAWMFALVGMNMLYFTRGKLTG 600
QY 601 TYSIMIOKILFKDLFFLLVYLLFMIGYASALVSLNCPANMKVCNEODNCTVPTPSC 660
D 601 TYSIMIOKILFKDLFFLLVYLLFMIGYASALVSLNCPANMKVCNEODNCTVPTPSC 660
QY 661 ROSEFTSTFLDLFKLTIGKMDLEMLSTKYPVVFIILLVYIILLFVLLINMLTAMGE 720
D 661 ROSEFTSTFLDLFKLTIGKMDLEMLSTKYPVVFIILLVYIILLFVLLINMLTAMGE 720
QY 721 TVGVSKESKHTWKLO 736
D 721 TVGVSKESKHTWKLO 736

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D 721 TVGVSKESKHTWKLO 736

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RESULT 11
US-10-027-828-2
; Sequence 2, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-828-2

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Query Match          99.2%; Score 3828; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 6.4e-305;
Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MADSSGPRAGPGEVAELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60
D 1 MADSSGPRAGPGEVAELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60
QY 61 GDRPMLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAMDSLFDYGYRHHSSDN 120
D 61 GDRPMLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAMDSLFDYGYRHHSSDN 120
QY 121 KWRKKIIEKOPSPAPAPQPPILKVENRPLIFDIVSGSTADLDGLPFLTHKKRL 180
D 121 KWRKKIIEKOPSPAPAPQPPILKVENRPLIFDIVSGSTADLDGLPFLTHKKRL 180
QY 181 TDEEFEPSTGTCCLPKALINSNGNDITPVLDIAERTGNRREFINSFPRDIYRGOT 240
D 181 TDEEFEPSTGTCCLPKALINSNGNDITPVLDIAERTGNRREFINSFPRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYGELPLSLAQTNPPI 300
D 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYGELPLSLAQTNPPI 300
QY 301 VVLTENPKKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDILLKCARLFPDS 360
D 301 VVLTENPKKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDILLKCARLFPDS 360
QY 361 NLEAVANNQGLSPLMMAATGKIGIPOHIIIRREVTDEDRHLSRKFKDWAYGVSISLD 420
D 361 NLEAVANNQGLSPLMMAATGKIGIPOHIIIRREVTDEDRHLSRKFKDWAYGVSISLD 420
QY 421 LSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDKWRKGAVSFYINVSYL 480
D 421 LSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDKWRKGAVSFYINVSYL 480
QY 481 AVVIFLTAAYQPLEBGTPPYPRRTVDYRLAGEVITLFTGVLFPTNKKDLFMKCPGV 540
D 481 AVVIFLTAAYQPLEBGTPPYPRRTVDYRLAGEVITLFTGVLFPTNKKDLFMKCPGV 540
QY 541 NSLFDGSPQLLYFYISVIVISAALYLAGIEAYLAWMFALVGMNMLYFTRGKLTG 600
D 541 NSLFDGSPQLLYFYISVIVISAALYLAGIEAYLAWMFALVGMNMLYFTRGKLTG 600
QY 601 TYSIMIOKILFKDLFFLLVYLLFMIGYASALVSLNCPANMKVCNEODNCTVPTPSC 660
D 601 TYSIMIOKILFKDLFFLLVYLLFMIGYASALVSLNCPANMKVCNEODNCTVPTPSC 660

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Db      601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Qy      661 RDESETSTFLDLFKLTIGMDLEMLSTCYPVVFIIILVYIIILFVLLNLMLALMGE 720
Db      661 RDESETSTFLDLFKLTIGMDLEMLSTCYPVVFIIILVYIIILFVLLNLMLALMGE 720
Qy      721 TVGQVSKESKHIWKLQ 736
Db      721 TVGQVSKESKHIWKLQ 736

RESULT 12
US-10-342-844-60
; Sequence 60, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Veilicelabi, G'n_1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAG28029
; DATABASE ENTRY DATE: 2000-10-31
US-10-342-844-60

Query Match      99.2%; Score 3828; DB 15; Length 871;
Best Local Similarity 99.9%; Pred. No. 6.4e-305;
Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MADSSEGPRAAGPGEVAELPGDESGTSGEAFPLSLANLFBGEDEGSLSPSPADASRPAGP 60
Db      1  MADSSEGPRAAGPGEVAELPGDESGTSGEAFPLSLANLFBGEDEGSLSPSPADASRPAGP 60
Qy      61  GDGRPNLRMKFOGAFRRKGVNPIDLLSTLYESSVVPKPKAPMDSLFDYGTYYHHSSDN 120
Db      61  GDGRPNLRMKFOGAFRRKGVNPIDLLSTLYESSVVPKPKAPMDSLFDYGTYYHHSSDN 120
Qy      121  KRWKPKKIIIEKQPSKPAAPQPPILKVFNRPILFDIVSRGSTADLDGLLPELLTHKKRL 180
Db      121  KRWKPKKIIIEKQPSKPAAPQPPILKVFNRPILFDIVSRGSTADLDGLLPELLTHKKRL 180
Qy      181  TDEFFRSTGKTCLPRALNLNSGRNDTIPVLLDIAERTGMREEFINSPPRDIIYRGQT 240
Db      181  TDEFFRSTGKTCLPRALNLNSGRNDTIPVLLDIAERTGMREEFINSPPRDIIYRGQT 240
Qy      241  ALHTAIRRCRGYVELLVAGADYHAQARGFFQPKDGGYFYFGEIPLSLAAGTNOPI 300
Db      241  ALHTAIRRCRGYVELLVAGADYHAQARGFFQPKDGGYFYFGEIPLSLAAGTNOPI 300
Qy      301  VNYITLTPHKKADMRDQSRNTVLAHALVALADTRETKEVTGMVYDILLIKCARLPDS 360
Db      301  VNYITLTPHKKADMRDQSRNTVLAHALVALADTRETKEVTGMVYDILLIKCARLPDS 360
Qy      361  NLEAVLNNDGLSPIMMAAKTGIGIHOHIIREVLTDEDETRHLSRKFQDMAYGPIYSSLYD 420
Db      361  NLEAVLNNDGLSPIMMAAKTGIGIHOHIIREVLTDEDETRHLSRKFQDMAYGPIYSSLYD 420

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Qy      421  LSLDLTCGEBAVLEILVYNSKIENHEMLAVPINELLJDKXKRGAVFYINVSYL 480
Db      421  LSLDLTCGEBAVLEILVYNSKIENHEMLAVPINELLJDKXKRGAVFYINVSYL 480
Qy      481  AMVIFTLTAYOPLBEGPPPYRTTYDYRLAEVITLTFGULFFFTNIDLPKKRQGV 540
Db      481  AMVIFTLTAYOPLBEGPPPYRTTYDYRLAEVITLTFGULFFFTNIDLPKKRQGV 540
Qy      541  NSLFDGSPQLLYFYISVAVIVSAALYAGIEAVLAVMWVAVLGMNVALYFRGLKLTG 600
Db      541  NSLFDGSPQLLYFYISVAVIVSAALYAGIEAVLAVMWVAVLGMNVALYFRGLKLTG 600
Qy      601  TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Db      601  TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Qy      661  RDESETSTFLDLFKLTIGMDLEMLSTCYPVVFIIILVYIIILFVLLNLMLALMGE 720
Db      661  RDESETSTFLDLFKLTIGMDLEMLSTCYPVVFIIILVYIIILFVLLNLMLALMGE 720
Qy      721  TVGQVSKESKHIWKLQ 736
Db      721  TVGQVSKESKHIWKLQ 736

RESULT 13
US-10-027-828-4
; Sequence 4, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeht, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL, PROTEIN, NUCLEIC ACIDS E
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-828-4

Query Match      99.1%; Score 3825; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 1.1e-304;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MADSSEGPRAAGPGEVAELPGDESGTSGEAFPLSLANLFBGEDEGSLSPSPADASRPAGP 60
Db      1  MADSSEGPRAAGPGEVAELPGDESGTSGEAFPLSLANLFBGEDEGSLSPSPADASRPAGP 60
Qy      61  GDGRPNLRMKFOGAFRRKGVNPIDLLSTLYESSVVPKPKAPMDSLFDYGTYYHHSSDN 120
Db      61  GDGRPNLRMKFOGAFRRKGVNPIDLLSTLYESSVVPKPKAPMDSLFDYGTYYHHSSDN 120
Qy      121  KRWKPKKIIIEKQPSKPAAPQPPILKVFNRPILFDIVSRGSTADLDGLLPELLTHKKRL 180
Db      121  KRWKPKKIIIEKQPSKPAAPQPPILKVFNRPILFDIVSRGSTADLDGLLPELLTHKKRL 180
Qy      181  TDEFFRSTGKTCLPRALNLNSGRNDTIPVLLDIAERTGMREEFINSPPRDIIYRGQT 240
Db      181  TDEFFRSTGKTCLPRALNLNSGRNDTIPVLLDIAERTGMREEFINSPPRDIIYRGQT 240
Qy      241  ALHTAIRRCRGYVELLVAGADYHAQARGFFQPKDGGYFYFGEIPLSLAAGTNOPI 300
Db      241  ALHTAIRRCRGYVELLVAGADYHAQARGFFQPKDGGYFYFGEIPLSLAAGTNOPI 300

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QY 301 VVLTENPHKKADMRQDSRGNTVHALVAIAADNTENTKFTVKMDLLILKCARLPDS 360
DB 301 VVLTENPHKKADMRQDSRGNTVHALVAIAADNTENTKFTVKMDLLILKCARLPDS 360
QY 361 NLEAVLNNDGLSPILMAAATGKIGIFQHIIRREVTDEDRHSRKFKDWAYGVYSSLYD 420
DB 361 NLEAVLNNDGLSPILMAAATGKIGIFQHIIRREVTDEDRHSRKFKDWAYGVYSSLYD 420
QY 421 LSSLDTCGEBASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSYINVSYL 480
DB 421 LSSLDTCGEBASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSYINVSYL 480
QY 481 AMVIFTLTAAYOPLBETPPYPTTYDYRLAGEVITLFTGVLPFTTNIKDLPMKKCPGV 540
DB 481 AMVIFTLTAAYOPLBETPPYPTTYDYRLAGEVITLFTGVLPFTTNIKDLPMKKCPGV 540
QY 541 NSLFDGSPQLLYFTYSVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600
DB 541 NSLFDGSPQLLYFTYSVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600
QY 601 TYSIMIQKILFQDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
DB 601 TYSIMIQKILFQDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
QY 661 RDSFTFTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720
DB 661 RDSFTFTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720
QY 721 TVGVSKESKHIWKLO 736
DB 721 TVGVSKESKHIWKLO 736

RESULT 14
US-10-090-215-7
; Sequence 7, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvart, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glaes, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/090,215
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-215-7

Query Match 99.1%; Score 3823; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 1.7e-304;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MADSEGRAPGGEVAELPGDESGTGGGEAPPLSLANLFGEDGSLSPSPADSRPAGP 60
DB 1 MADSEGRAPGGEVAELPGDESGTGGGEAPPLSLANLFGEDGSLSPSPADSRPAGP 60
QY 61 GDGRPNLMKFOGAFKRVGNPIDLLESTIYESSVVPKPAKPMQSLFDYGYRHSSDN 120
DB 61 GDGRPNLMKFOGAFKRVGNPIDLLESTIYESSVVPKPAKPMQSLFDYGYRHSSDN 120
QY 121 KRMKKTIEKOPQSKAPAPPPPIIKVFNRPPIIDIVSRGSTADLGLPFLTHKKRL 180
DB 121 KRMKKTIEKOPQSKAPAPPPPIIKVFNRPPIIDIVSRGSTADLGLPFLTHKKRL 180
QY 181 TDEEFREPSGTGTCPLKALLNLSNGRNDTIPVLLDIARTGNMFEFINSPPRDIYYRGOT 240
DB 181 TDEEFREPSGTGTCPLKALLNLSNGRNDTIPVLLDIARTGNMFEFINSPPRDIYYRGOT 240

DB 181 TDEEFREPSGTGTCPLKALLNLSNGRNDTIPVLLDIARTGNMFEFINSPPRDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVQAGDVHAQAGRFQPDDEGYFFFGELPLSLACTQPHI 300
DB 241 ALHIAIERCKHYVELLVQAGDVHAQAGRFQPDDEGYFFFGELPLSLACTQPHI 300
QY 301 VVLTENPHKKADMRQDSRGNTVHALVAIAADNTENTKFTVKMDLLILKCARLPDS 360
DB 301 VVLTENPHKKADMRQDSRGNTVHALVAIAADNTENTKFTVKMDLLILKCARLPDS 360
QY 361 NLEAVLNNDGLSPILMAAATGKIGIFQHIIRREVTDEDRHSRKFKDWAYGVYSSLYD 420
DB 361 NLEAVLNNDGLSPILMAAATGKIGIFQHIIRREVTDEDRHSRKFKDWAYGVYSSLYD 420
QY 421 LSSLDTCGEBASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSYINVSYL 480
DB 421 LSSLDTCGEBASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSYINVSYL 480
QY 481 AMVIFTLTAAYOPLBETPPYPTTYDYRLAGEVITLFTGVLPFTTNIKDLPMKKCPGV 540
DB 481 AMVIFTLTAAYOPLBETPPYPTTYDYRLAGEVITLFTGVLPFTTNIKDLPMKKCPGV 540
QY 541 NSLFDGSPQLLYFTYSVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600
DB 541 NSLFDGSPQLLYFTYSVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600
QY 601 TYSIMIQKILFQDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
DB 601 TYSIMIQKILFQDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
QY 661 RDSFTFTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720
DB 661 RDSFTFTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720
QY 721 TVGVSKESKHIWKLO 736
DB 721 TVGVSKESKHIWKLO 736

RESULT 15
US-09-932-165-1477
; Sequence 1477, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALITRA-ELD, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFERAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENNE
; APPLICANT: GE, WANGMAO
; TITLE OF INVENTION: NOCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2H1 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1477
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURES:
; OTHER INFORMATION: Description of Unknown Organism: CatF2H1
US-09-932-165-1477

Query Match 98.8%; Score 3810; DB 10; Length 963;

Best Local Similarity 99.6%; Pred. No. 2.3e-303;
Matches 733; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MADSSGPPAGGAEVAELPGDESGTPGGAPLSSLANLFEGBDGSLSPPADASRPAGP 60
Db 93 MADSSGPPAGGAEVAELPGDESGTPGGAPLSSLANLFEGBDGSLSPPADASRPAGP 152
QY 61 GGRPRLRMKPGQAPRKGVNPIDLESTLYESSVPGPKKAPMDSLFDYGYRRHSSDN 120
Db 153 GGRPRLRMKPGQAPRKGVNPIDLESTLYESSVPGPKKAPMDSLFDYGYRRHSSDN 212
QY 121 KEMRKXIIIEKOPQSPKAPAPPEPILKVENRPLFDIVSRGSTADLDGLLPILLTHKKRL 180
Db 213 KEMRKXIIIEKOPQSPKAPAPPEPILKVENRPLFDIVSRGSTADLDGLLPILLTHKKRL 272
QY 181 TDEEFPREPSTGKTCLEPKALINLNGNDTIPVLLDIAERTGMREFINSPPFDIYYRGQT 240
Db 273 TDEEFPREPSTGKTCLEPKALINLNGNDTIPVLLDIAERTGMREFINSPPFDIYYRGQT 332
QY 241 ALHIAIERRCKHYVELLVAQADVHAQAGRPFPQPKDEGVEFYFGEPLSLAACTNQPHI 300
Db 333 ALHIAIERRCKHYVELLVAQADVHAQAGRPFPQPKDEGVEFYFGEPLSLAACTNQPHI 392
QY 301 VNYLTENPKKADMRRODSRGNTVLAALVAIADNTRENTKVTXMYDILLKCARLPDS 360
Db 393 VNYLTENPKKADMRRODSRGNTVLAALVAIADNTRENTKVTXMYDILLKCARLPDS 452
QY 361 NLEAVINNGSLPIMAAKTGKIGIHOHIIREVTEDETRHLSRKFKDWAYGVPYSSLYD 420
Db 453 NLEAVINNGSLPIMAAKTGKIGIHOHIIREVTEDETRHLSRKFKDWAYGVPYSSLYD 512
QY 421 LSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELRDKWRKFGAVSFYINVSYLQ 480
Db 513 LSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELRDKWRKFGAVSFYINVSYLQ 572
QY 481 AMVIFTLTAYYOPLBGTPPYRPTVDYLRLAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540
Db 573 AMVIFTLTAYYOPLBGTPPYRPTVDYLRLAGEVITLFTGVLPFTNLIKDLFMKKCPGV 632
QY 541 NSLFIQSGPQLLYFIYSVLYIVSAALYLAGIEAYLAMVAFALYGMWMLLYFTRGKLTG 600
Db 633 NSLFIQSGPQLLYFIYSVLYIVSAALYLAGIEAYLAMVAFALYGMWMLLYFTRGKLTG 692
QY 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Db 693 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 752
QY 661 RDSETPSTFLLDLFEKLTIGMDLEMLSTYYPVFIIILVTYIILTFVLLINMLIALMGE 720
Db 753 RDSETPSTFLLDLFEKLTIGMDLEMLSTYYPVFIIILVTYIILTFVLLINMLIALMGE 812
QY 721 TVGQVSKESKHIMKLQ 736
Db 813 TVGQVSKESKHIMKLQ 828
```

Search completed: December 2, 2004, 22:39:18
Job time : 152 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:17:36 ; Search time 44 Seconds

(without alignments)
1622.565 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSEGPRAQGEVALPLPG.....GVSKSKHMKLQSGRRRL 742

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1579.5	40.9	838	2	T09054
2	1551.5	40.2	839	2	T09054
3	736.5	19.1	727	2	JC7796
4	724.5	18.8	725	2	JC7531
5	719	18.6	723	2	JC7795
6	473.5	12.3	937	2	T37241
7	473.5	12.3	957	2	D88651
8	435.5	11.3	900	2	T33026
9	313.5	8.1	790	2	T20312
10	278	7.2	519	2	T24772
11	204.5	5.3	1188	2	T19552
12	188	4.9	828	2	UC5807
13	145.5	3.8	1124	2	JH0588
14	138.5	3.6	810	2	I38361
15	137	3.6	616	2	T00894
16	137	3.6	1765	2	T42388
17	136.5	3.5	683	2	A85044
18	136	3.5	2352	2	J30201
19	134	3.5	1275	2	JU0092
20	133	3.4	481	2	T23729
21	132	3.4	1274	2	JN0015
22	131.5	3.4	642	2	S88154
23	130.5	3.4	652	2	D85044
24	129.5	3.4	608	2	G02640
25	129	3.3	823	2	S44873
26	127.5	3.3	4377	2	A55575
27	126.5	3.3	643	2	D86167
28	126.5	3.3	2471	2	A49128
29	126	3.3	2212	2	A41098

30	125.5	3.3	934	1	H71274	probable ankyrin -
31	125.5	3.3	2529	2	B64635	toxin-like outer m
32	125	3.2	1957	2	S68453	sodium channel pro
33	124	3.2	793	2	S68238	trp-1 protein - nu
34	123.5	3.2	968	2	A37867	transcription fact
35	123	3.2	751	2	F85043	hypothetical prote
36	123	3.2	2531	2	T31070	notch homolog - se
37	121	3.1	488	2	JC7995	transient receptor
38	121	3.1	1549	2	T13940	ankyrin - fruit fl
39	120.5	3.1	397	2	T46445	hypothetical prote
40	120.5	3.1	573	2	D86464	Fl2612.13 protein
41	120.5	3.1	664	2	A56695	notch2 protein hom
42	120	3.1	633	2	T27499	hypothetical prote
43	119.5	3.1	574	2	T47566	hypothetical prote
44	119	3.1	1765	2	T42714	ankyrin 3' splice
45	119	3.1	1940	2	T42715	ankyrin 3' splice

ALIGNMENTS

RESULT 1

T09054
capsaicin receptor - rat
N.Alternate names: vanilloid receptor subtype 1
C.Species: Rattus norvegicus (Norway rat)
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C.Accession: T09054
R.Caterina, M.D.; Schumacher, M.A.; Tomimaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D.
Nature 389, 816-824, 1997
A.Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.
A.Reference number: Z16539; MUID:98007969; PMID:9349813
A.Accession: T09054
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-838 <CAT>
A.Cross-references: UNIPROT:O35433; EMBL:AF0293310; NID:G2570932; PIDN:AA053398.1; PID:G
A.Experimental source: dorsal root ganglion
A.Keywords: ion channel; receptor

Query Match	40.9%	Score 1579.5;	DB 2;	Length 838;
Best Local Similarity	44.6%	Pred. No. 1.1e-103;		
Matches	338;	Conservative 129;	Mismatches 193;	Indels 97; Gaps 16;
QY	16	AEIPGDESGTGGG-----APPLSLANLFEEDGSLSPSPADA	54	
DB	5	ASLSESESESPQENSCLDPPDRDNCPPPVKPHITFRSRTRLF-GKGDSEASPLDC	63	
QY	55	SRPAGPGDGRNLRMKFGQAFKGVPN-PIDLESTLYESSVVGPKKAPMDSLFDYGTV	113	
DB	64	FYERG-----GLASCPITTVSSVL-----TIQRPGDG-----ASV	94	
QY	114	RHHSNDNRMRKRIIEKOPSPKAPAPOPPPILVFNFPPIIFDVISRGSTDLGLPFL	173	
DB	95	RPSSQDS-----VSAGEKPP--FLYRRRSIFDVAQSCCELSLPLPFL	136	
QY	174	LTHKKRLDEERFREPSTGKTCLPKALNLSGRBDTIPVLDIERTGNBEPFNSPPRD	233	
DB	137	QRSKKRLTDSFKPDEFGKTCILKAMLNHNGDDTILALNDVARKDLSLQFVNASYTD	196	
QY	234	IYRQGTLAIAIRERCKHYVELLVAQADVAHAQARFQPKDGGYFEGELPLSLAA	293	
DB	197	SYRGQPLAIAIRRRMMTLVTLVENGADVOAANGDFPFKTKGRPGFYGEPLSLAA	256	
QY	294	CTNCPHIVNYITENPHKKAKRRODSKGNVYLAHALVAIDNTREYTKVTKYDILLKLC	353	
DB	257	CTNOLAIVKFLIQQNSWQPADISARSDVGNVLAHLVEVADVTNTKFTVNTMYNEILLIG	316	
QY	354	ARLPDSNLBAVLNNDGSLPMLMAAKTGKIGIPHHIRREVTDDTRHLSKPKDWAYGP	413	
DB	317	AKHPTLKLBEITNRKGIITPLATASSGKIGVLAIVYQREHRECHLSKFTFEMAYGP	376	
QY	414	VYSLYLDSIDTCGEASVLEILVY-NSKIENHEMLAVEPINELLDRKRRKGAVSFY	472	

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Db      377 VHSLSYDLSCLDTC-EKNSVLEVIAYSSSETPNRHDMVLVEPLNLLQDKMRPFVKRIEY 435
QY      473 INVSYLCAMVITFTLTANYQPLEGTPPYRYRTTV-DYLRAGEVITLTFGLVFETTNIKD 531
Db      436 FNFPPCYLYMIFLTAAYAYRPEGLPKNTVADYFVLTSEILSVSGGVFFFRGIG- 494
QY      532 LFMKCPGVNSLFIQSGFOLLYFYISVLYVISAALYAGIEAVLYAMVPEALVGMNNAIY 591
Db      495 YTLQGRPSIKSLFVDSYSILFVQSLFPLVSVLYFSGRKRYVASMVPYSLAMGWTNNIY 554
QY      532 FTRGLKLTGTYSIMTOKILFKDLFRLVLYLLFMIGYASALVSLNPPCANMKVCNEDQTN 651
Db      555 YTRGFQMGITVAMIEKMLIRDLCRFMFYLVFLFGFTAVVTLI-----EDGKN 604
QY      652 CLVP---LYPSGRDS-----EFTFELLDFLTITGMGDLMLSTKXPVVFITL 699
Db      605 NSLPMSSTPHKRGSGCKRGNSYNSLYST-CLELFFFTITGMGDLFTFTENYDKAVFILL 663
QY      700 VTYYITLFTVLLNMLIALMGFTVGVSKESKHIMKIQ 736
Db      664 LAVVILITVLLNMLIALMGFTVKNKIAQSKNIMKIQ 700

RESULT 2
JC7621
capsaicin receptor, VR1 - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07621
R/Corr/Right, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A/Title: The tissue distribution and functional characterization of human VR1.
A/Reference number: J07621; PMID:11243859
A/Comments: Dorsal root ganglia
A/Accession: J07621
A:Molecule type: mRNA
A:Residues: 1-839 <COR>
A/Cross-references: UNIPROT:Q9H304; GB:AF196175
C/Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a
    lie integrative activation by several noxious stimuli, and plays an important role in in
    C/Genetics:
A/Genes: VR1
A/Map position: 17p13
C/Keywords: transmembrane protein
F/201-233/Domain: ankyrin #status predicted <ANK1>
F/248-280/Domain: ankyrin #status predicted <ANK2>
F/333-365/Domain: ankyrin #status predicted <ANK3>
F/333-455/Domain: transmembrane #status predicted <TM1>
F/477-495/Domain: transmembrane #status predicted <TM2>
F/508-531/Domain: transmembrane #status predicted <TM3>
F/543-569/Domain: transmembrane #status predicted <TM4>
F/578-597/Domain: transmembrane #status predicted <TM5>
F/624-644/Region: pore loop #status predicted
F/656-684/Domain: transmembrane #status predicted <TM6>

Query Match 40.2%; Score 1551.5; DB 2; Length 839;
Best Local Similarity 44.4%; Pred. No. 1,1e-101;
Matches 320; Conservative 138; Mismatches 189; Indels 74; Gaps 12;

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Db      174 IPLLLEIARQDSDLSKELVNASSTDSYVGOTALHAIERRRNALVTLIVENADVAQAAN 233
QY      270 GRFPQKDEGGYFYFGEPLSLIAACTNOPIHYNYLTENPHKKADMRPODSRNTVLAHY 329
Db      224 GDFPKTKGRPGFTYGEPLSLIAACTNOGLVFKLLQNSWCQADISARDSVNTVLAHY 293
QY      330 ALADNTRENTKVTMYDILLKCARLFPDSNLEAVLNNDGLSPMLMAAKTKIGI FOHI 389
Db      294 EVADNTADNTKVTSMYNEIIMLAGLHPHTLLEELTKKKGWTPALAACTKIGVLAHY 353
QY      390 IRRVTEDETRLSKFKDMAAGPYSSLYDLSLDTGCEBSVLEIIVY-NSKLENRHE 448
Db      354 LQRELOEPCRHLSKRFEMAGPVHSSLYDLSCLDTC-EKNSVLEVIAYSSSETPNRHD 412
QY      449 MAAVPEIHELADKKRKFGAVSYINVSYLCAMVITFTANYQPLEGTPPYRYRTVDY 508
Db      413 MLVPEPLRLQDKDRPFVKRIEYFNFLVYCYLMIIFTMAAYRPPVDGLPFRMEKIGDY 472
QY      509 IRLAGEVITLFTGLVFETTNIKDLFMKCPGVNSLFIQSGFOLLYFYISVLYVISAALY 568
Db      473 FVYTGELISLVGGVYFFFRGIG-YELQRRSPSKTLFVDSYSMLFPLQSLFMLATVLYF 531
QY      569 AGIEAVLYAMVPEALVGMNNAIYFTRGLKLTGTYSIMTOKILFKDLFRLVLYLLFMIGY 628
Db      532 SHKREYASWVPSLALGMNTMLYTRGFQMGITVAMIEKMLIRDLCRFMFYIYVFLRGF 591
QY      629 ASALVSLNPPCANMKVCNEDQTNCTVPTY-----PSCRDSST-----FSTFLIDLPK 675
Db      592 STAVVTLI-----EDGKNDSLPSSTSHRMGPAKRPDSSYNSLYST-CLELPRK 640
QY      676 LITGMGDLMLSTTYKPVVFILLVYITLTVLLNMLIALMGFTVGVSKESKHIMKIQ 735
Db      641 FTIGMGDLFTFTENYDFKAVFIILLAVYITLTVLLNMLIALMGFTVKNKIAQSKNIMKIQ 700
QY      736 Q 736
Db      701 Q 701

RESULT 3
JC7796
epithelial calcium channel 2, ECAC2 - mouse
N/Alternate names: calcium T1; CaT1
C/Species: Mus musculus (house mouse)
C/Date: 02-Apr-2002 #sequence_revision 17-May-2002 #text_change 09-Jul-2004
C/Accession: J07796
R/Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A/Title: Gene structure and regulation of the murine epithelial calcium channels ECAC1 a
A/Reference number: J07795
A/Accession: J07796
A:Molecule type: DNA
A:Residues: 1-727 <WEB>
A/Cross-references: UNIPROT:Q91WP2; GB:AF336378
C/Comment: This calcium channel plays an important role in active transcellular calcium
    relevant for in vivo calcium homeostasis.
C/Genetics:
A/Genes: ECAC2
A/Map position: 6
A/Intons: 43/2; 76/1; 117/1; 163/1; 196/1; 253/3; 302/3; 373/3; 402/3; 428/2; 483/3; 50
C/Keywords: calcium channel

Query Match 19.1%; Score 736.5; DB 2; Length 727;
Best Local Similarity 33.3%; Pred. No. 4,4e-44;
Matches 196; Conservative 101; Mismatches 193; Indels 99; Gaps 21;

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Db      120 ALHIAVINQNVNVLVRLALLARGASVSARATGVSFVHFRPH-NLIYGEHPLSFAACVGSSEI 178
Qy      301 VNYLTENPKKADMRQDSRGNTVLAHALVADNTEENTKFTVTKWDL-----LKC 353
Db      179 VKLLIEH---GADIRQDSLGNVTIHL-----LQPNKTFACQMNLLSIDGGHDK- 229
Qy      354 ARLPDSNLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVTDETRHLSRKFKWYAGP 413
Db      230 -----SLELVPNNQGLTFPKLAGVEGNI VNFQHLMOK-----RKHQWYGP 271
Qy      414 VYSLSYDSSLDTCGEASVLELIVYNSKIENHEMLAVPINELDRKRFAGVAFYI 473
Db      272 LSTSLTLEIDSSGDSGLLELIVTKRKREAR-QILDDTPVKEISLWKMKRGREYFCV 330
Qy      474 NVVSYLCAMVITFLTAAYQPLE-----GTRP-----YPRRTVDYRLAGEVI 516
Db      331 LGALVYLYIICFMCCVYRPLKERTNRKTRNPRDNTLMQOKLQEAATVPEDDLRLVGEIV 390
Qy      517 TLTGVLFFFTNIKIDLFMKKCPGVNSLF-----IDGSFQLLYFYSLVIVISAALYLAGIE 572
Db      391 STVGAVIILLLVELPIDFRL---GVTRFPGQTLIGSFPHVILITVAFMVLTVMRLTNDV 447
Qy      573 AVALAVPVLVGMNALYFTRGKLTGYYSIMIOKILFKDLFRFLVILLEMIGYASAL 632
Db      448 GEVVPMSFALVIGCMVWYFARGFQMLGFTTMIQKIFGDLRFQMLMAVVLIGFASAF 507
Qy      633 VSLNLCAMKVCNEDQTC-TVTPYPSCHDSETFSTFLDLFKLTIGMG---DLEMIS 687
Db      508 YIIFQ-----TEPDELGHFYDPM-----LFTSF-ELF-LTIIDGPANYVDL- 550
Qy      688 STEYVVFILLVYIILTFVLLNMLALMGETVQVSKSHIKLO 736
Db      551 ----PMTSVTYAFAIATLMLNLMLMGDTMHRVAHERDELWRAQ 595

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RESULT 4
JC7531
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7531
R:Peng, J.B.; Chen, X.; Berger, U.V.; Wieremowicz, S.; Morton, C.C.; Vassilev, P.M.; Brown
Biochem. Biophys. Res. Commun. 278, 326-332, 2000
A:Title: Human calcium transport protein Cat1.
A:Reference number: JC7531; MIMD:20551480; PMID:11097838
A:Accession: JC7531
A:Molecule type: mRNA
A:Residues: 1-725 <PDB>
A:Cross-references: UNIPROT:Q9H296; GB:AF304463
C:Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular
line and kidney.
C:Genetics:
A:Gene: Cat1
A:Map position: 7q33-34
C:Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

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Query Match      18.8%; Score 724.5; DB 2; Length 725;
Best Local Similarity 32.9%; Pred. No. 3,1e-43;
Matches 198; Conservative 99; Mismatches 218; Indels 87; Gaps 20;

Qy      171 PFLTHK-----KELTDEER--EPSTGKTCLPKALL--NLSGRNDTIPVLIDIA 217
Db      48 PILLAKDNVQALNKLKYEDCKVHRGAMGETALHIALYDNL-----EAMVIMBEAA 102
Qy      218 ERKGNMREFFNSPRDIYRGQTLAHIAIERCKHYVELVAQADVHAQARGFPQPKD 277
Db      103 P-----ELVFEPTTSELVYGQTLAHIAVNNNNLVRALLARASVSARATGAFR-RS 155
Qy      278 EGGVYFGEPLSLAACLTPQPHIVNYLTENPHKADMRQDSRGNTVLAHALVADNTR 337
Db      156 PCNLIYGEHPLSFAACVGSSEIYVLLIEH---GADIRQDSLGNVTIHLI-----LQ 207
Qy      338 NTKFVTNMDLLILKCARLPDSNLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVTDE 397

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Db      208 NTKFACQWYNLLISYDRHGHLPDLVFNHQGLTFPKLAGVEGNTVMFOHLMOK----- 262
Qy      398 DTRHLSRKFKDWAGPVVYSLSYDSSLDTCGEASVLELIVYNSKIENHEMLAVPINE 457
Db      263 -----RKHQWYGPDLSTLYDLREIDSSGDSGLLELITTKRKREAR-QILDDTPVKE 315
Qy      458 LTRDKRKREKAVSFYINVSYLCAWITFLTAAYQPLE-----GTRP-----Y 500
Db      316 LVSLMKMKRGREYFCMLGALVLYIICFMCCVYRPLKERTNRKTRNPRDNTLMQOKLQ 375
Qy      501 PYRTVDYRLAGEVITLFTGVLFFFTNIKIDLFMKKCPGVNSLF-----IDGSFQLLYFY 556
Db      376 AMTPEDDLRLVGEIVTVAIGALIIILVEPDIFFRM---GVTRFPGQTLIGSFPHVILITY 432
Qy      557 SVLVYSALYLAGIEAVLVAVWVPLVGMNALYFTRGKLTGYYSIMIOKILFKDLFR 616
Db      433 AFVAVLTVMWRLISASGEVPMSPALVLCMNVYFARGFQMLGFTTMIQKIFGDLRF 492
Qy      617 FLTVYLIFMIGYASALVSLNLCAMKVCNEDQTC-TVTPYPSCHDSETFSTFLDLFK 675
Db      493 FCMMAVVLIGFASAFYIIFQ-----TEPDELGHFYDPM-----LFTSF-ELF- 537
Qy      676 LTIIGMDLEMSSTKTPVFIILVYIILTFVLLNMLALMGETVQVSKSHIKWL 735
Db      538 LTIIDGPANY--NVDLPFYISITYAFAIATLMLNLMLMGDTMHRVAHERDELWRA 595
Qy      736 Q 736
Db      596 Q 596

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RESULT 5
JC7795
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C:Accession: JC7795
R:Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A:Title: Gene structure and regulation of the murine epithelial calcium channels ECa1
A:Reference number: JC7795
A:Accession: JC7795
A:Molecule type: DNA
A:Residues: 1-723 <WEB>
A:Cross-references: GB:AF336378
C:Comment: This calcium channel plays an important role in active transcellular calcu
relevant for in vivo calcium homeostasis.
C:Genetics:
A:Gene: ECa1
A:Map position: 6
A:Intons: 37/2; 70/1; 111/1; 157/1; 190/1; 247/3; 296/3; 367/3; 396/3; 422/2; 477/3;
C:Keywords: calcium channel

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Query Match      18.8%; Score 719; DB 2; Length 723;
Best Local Similarity 33.3%; Pred. No. 7.6e-43;
Matches 201; Conservative 100; Mismatches 198; Indels 104; Gaps 23;

Qy      173 LTHKKRLNDE--EPRE-PSGKTCLPKALL--NLSGRNDTIPVLID-----IAERTGN 222
Db      52 MCTLKQLQHDQNCDFRQCALGETALHVALYDNL-----DAIMTMEAPLYVTEST-- 104
Qy      223 MREFFNSPFEDIIYRGQTLAHIAIERCKHYVELVAQADVHAQARGFPQPKDEGGYF 282
Db      105 ----LQEP-----VQGTALHIVMNNVNLVRLALLARGASASARATGSAFH-RSSHNL 154
Qy      283 YFGEPLSLAACLTPQPHIVNYLTENPHKADMRQDSRGNTVLAHALVADNTRNKFV 342
Db      155 YFGEHPLSFAACVGSSEIYVLLIEH---GADIRQDSLGNVTIHLI-----LQPNKTF 206
Qy      343 TKWYDILL-----LKCARLPDSNLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVT 395
Db      207 CQMNLLISYDGGHDK-----SLELVPNNQGLTFPKLAGVEGNTVMFOHLMOK--- 255

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QY 396 DEDTRHLSRKKFEDNAGVGVSSLYDLSLDDCGEASVLEILVYNSKIENHEMLAAVEPI 455
Db 256 -----RGIQMSFGPILTSLYDLTLEIDSGEELSTLELVSSKKEAR-QILLEGTPV 306
QY 456 NELLKDKRKFGVASFYINVSZYLCAWIFLTLAYOPL-----EGTP 498
Db 307 KELVSLKHKKKQGFPECLLGALYIPYWCFTCCYRLKRDNRNRTHVDRNTIMEQSXL 366
QY 499 EYPRRTYDYLRLAGEVITLFTGVLPFTTNKDLFMKKCPGVNSLF---IDGSFOLIYF 554
Db 367 QEAAYTYODKRLVGEELTVIGAVIILLELPIER--VGASRYFGQTVLGPHEVYII 423
QY 555 IYSVLVYSALALTYAGTFAVLAVWFAVLVGMNANLYFTREGIKLTGYSTIMIOKILFODL 614
Db 424 TYASIVLITTMARLITNVGEEVPMFMAVLVGMCSWYFARGFOMLGPPTIMIOKIFGDL 483
QY 615 FRFLVLYLFFMIGYASALVSLINPCANMKVCNEDOTNC-TVPTYPSGCDSEFTSFLLDL 673
Db 484 LRFCLIMAMVILGSPASAFYIIFO-----TEBDNIDGESDPTFA---MFSTF-EL 529
QY 674 FKLITIGMDLEMLUSTKYPVVFIILVYIILFTVLLNMLIALMGEVGVGSXESKHIW 733
Db 530 F-LITIDGPANY--RVLDLRFMYSVTYATFALITATLMLNLFIAWNGDTHRWVAQERDELW 586
QY 734 KLOQ 736
Db 587 RAQ 589

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RESULT 6

T37241
olfactory channel protein osm-9 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37241
R/Colbert, H.A.; Smith, T.L.; Bargmann, C.I.
J. Neurosci. 17, 8259-8269, 1997
A/Title: OSM-9, A novel protein with structural similarity to channels, is required for
A/Reference number: N21639; MUID:97477445; PMID:9334401
A/Accession: T37241
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-937 <COL>
A/Cross-references: UNIPROT:O17469; EMBL:AF031408; NID:g2c42589; PIDN:AAB87064.1; PID:g2c42589
C/Genetics:
A/Gene: osm-9
A/Map position: IV
A/Keywords: transmembrane protein

Query Match	12.3%	Score 473.5	DB 2	Length 937
Best Local Similarity	27.1%	Pred. No. 2.6e-25		
Matches	149	Conservative 90	Mismatches 213	Indels 97
			Gaps	17

QY	233	DIYR---	GOTALHAIERCKHYVELLYAQAQDVHAQARFRPQK-----	DEG	279
Db	163	DIYGBQFQSOAHLAIVDDDEYVSLNLSKADVNARACGNFLEDEPKITNKIDYQ			222
QY	280	GFEYFGEPLSLACTQPHIVNYLITE---	NPHKAMRRQDSKGNVLAHALVAADNR		336
Db	223	GVAAYGEYELAPAACFQNKDIYDELLIQGANPN-----	LQDSGNIIIMCV-----		269
QY	337	ENKFFVTKMVDLLILKCARLFPDSNLEAVANNQGLSLPMAAKTGKIGIQHIIIREVTD			366
Db	270	--INYSSTMSYVAHMAK--PAD--	PHVNHAGFTLLATKIGRKOIPEEMLE----		318
QY	397	EDTRHLSRKRDMAAYGVYSIYDLSLSDICGEASV----	LEILVNSKLENRHEMLAV		452
Db	319	-----IMKVEFRFSDMTCSAVPLNTLDTIIGDGSINYSALMTVINSGSTPHLMDIGS			372
QY	453	EPINELLRDCKRKGFGAVSFYINVSYLCAWVITFLTYIYQPLLESTPYPRYRTV--	DYL		509
Db	373	EVYQRLADMKPAQKRLIERVLLIVQILITISIVYIAPTE--	PLRLMEDPQMDYI		430

[illegible]

RESULT 7

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D88651
Protein B0212.5 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88651
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2019, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A/5000; MUID:19069613; PMID:9851916
A:Note: See websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published extra appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88651
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-957 >STO>
A:Cross-references: UNIPROT:O17469; GB:chr_IV; PDB:AAO2569.1; PDB:92854148; GSPDB:GN00
C:Note: contains similarity to ankryrin repeats
C:Genetics:
A:Gene: B0212.5
A:Map position: 4

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[illegible]

Db 486 ----LTCIFRLMKHEIEE--ALFVFPALPGSMWILFEPARSAKLTGPFVQMIVSMIAGD 539
 QY 614 LERFLVYLTFMIGVASALVSL--LNP CANMKVCNEDQNTC-----TVPYPSCSRSEFS 667
 Db 540 MRFALISAFIVSSQVFPYFGKMDAKOKLEDNPNACRISGTYITY-----NTPP 593
 QY 668 TFLDLFKLTIGMDLEMLSTKYPVFIILLVYIITFVLLNMLTALMGETVGVSK 727
 Db 594 EFTFLTFRASMGGDYEEFS CANYOALTKTLFVLVMPFVPMIMINILLAMGNTTYTIVA 653
 QY 728 ESKHIMKIO 736
 Db 654 QAEKAMRQ 662

RESULT 8

T33026
 hypochelical protein T09A12.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T33026

R:Hawkins, J.; Fulcon, B.; Gilliam, B.
 submitted to the EMBL Data Library, February 1998
 A:Description: The sequence of C. elegans cosmid T09A12.
 A:Reference number: 221265

A:Accession: T33026

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-900 <HAM>

A:Cross-references: UNIPROT:O61220; EMBL:AF047660; PDB:1AC0431.1; GSPDB:GN00022; CESP:
 A:Experimental source: strain Bristol N2; clone T09A12

C/Genetics:

A:Gene: CESP:T09A12.3

A:Map position: 4

Query Match 11.3%; Score 435.5; DB 2; Length 900;
 Best Local Similarity 24.9%; Pred. No. 1.2e-22;
 Matches 167; Conservative 99; Mismatches 23; Indels 173; Gaps 26;

QY 189 STGTCTCPKALINLSNGNDITPVLLDIAERTGMREINSFPRDIY---YRGOTALHI 244
 Db 154 SMGETITIGCCLLHSDINNALVILKLDYPRILN-----DIHISEDYFGISPLHQ 203
 QY 245 A-IERRCHGYELVAQADVAHAQARGRFQPKDE-----GSGYF 282
 Db 204 AIIITDCK-LVYKPLKLGADVNSKCYGAFCAADQKASRTSLHEHYELSLKNTYTM 262
 QY 283 YFGLPISLAACNQHPIVNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKTV 342
 Db 263 YLGEYPLSFAACLNQPEFRLILA--FKANPNAQDTGNSVILHMCV-----IHENMAWF 314
 QY 343 TKMTVDLLIKCARLEPDSNLEAVLNNDGLSPLMAAKTKIGIGIQTIRREVTBEDTRHL 402
 Db 315 K-----LALREG-----ASLRTV-NKOSLSPLTLAAKAKKEMDEILLEGDSV----- 358
 QY 403 SRKFKDAAAGPVYSIVDLSLDTCGE-----EASVLEILVYNSKIENRHEMLAVEPIN 456
 Db 359 -----WAGDASSATAPLAKIDITINETGELNRSALSLVYVGYTVE--HELLIDGLLD 410
 QY 457 ELLRDKMRKFG---AVSFYINVSYSICAMVIFTL-----TAYYQPLEG- 496
 Db 411 TLLEAKNBAFAKRMNIVSFTAFPLYICFVTAFLIRPIGFTSTEMLTGEMINRYSEBPRGR 470
 QY 497 -----TPPYRYTYDYRLAGE---VI 516
 Db 471 YGNKSTIQQKVPVINAATSGVSESEPLISQCHLNWDPIPEANS--YIRLVFELFVVI 528
 QY 517 TLFTGVLEFFTNIDLPFKKCPGVNSLP-IDGSFQLYFIVSVIVYSAALYLAGIAYVL 575
 Db 529 GICGVVPLDFRDIKRIKRWKMMNVLTAPPAKITFRLTYFLVLAAMIPLRLACDLSPLVIV 588

QY 576 --AVWFAVLGWMNATLYTRGLKLTGTYSIMIQIKLEPKDLERFLVYLTFMIGVASALV 633
 Db 589 DNVLITVMTITVYHVLVYGVIRVGVFVLMVYIITNDIFRFLIYICIFLMGSGSIS 648
 QY 634 SLNDC--AN-MKVCNEDQNTC-----VPTYPSC--RDETFPS----- 667
 Db 649 LIFLSCERANVIKLITDOSEASESGSDNKNLTROIASAYDIAVKNANVEFENWQSPIE 708
 QY 668 ----TFLDLFKLTIGMDLEMLSTKYPVFIILLVYIITFVLLNMLTALMG--EE 720
 Db 709 AFVFTFLITGSEFVLYNRLALCPANVWIGKOVFIIFELFVSTIMQFNMLAMTRYE 768
 QY 721 TVGVSKESK 730
 Db 769 TIFOTGLEKX 778

RESULT 9

T20312
 hypochelical protein F28H7.10 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T20312

R:Mathews, P.
 submitted to the EMBL Data Library, June 1996

A:Reference number: Z19255

A:Accession: T20312

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-790 <WII>

A:Cross-references: UNIPROT:P90784; EMBL:Z74030; PDB:1CA98449.1; GSPDB:GN00023; CESP:F
 A:Experimental source: clone D1054

R:Berkas, M.
 submitted to the EMBL Data Library, May 1996

A:Reference number: Z19435

A:Accession: T21533

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-790 <WII>

A:Cross-references: EMBL:Z72508; PDB:1CA96644.1; GSPDB:GN00023; CESP:F28H7.10
 A:Experimental source: clone F28H7

C/Genetics:

A:Gene: CESP:F28H7.10

A:Map position: 5

Query Match 8.1%; Score 313.5; DB 2; Length 790;
 Best Local Similarity 22.0%; Pred. No. 4.4e-14;
 Matches 155; Conservative 94; Mismatches 209; Indels 245; Gaps 28;

QY 152 PILFDIVSRGSTALDGLLPFLTHKKRL-----TDEFRF-----PSYK 192
 Db 109 PNILDEPDQO-ALMAADL-----KRALKLLDGGKGSSEKTRKRWVMSVDEBSNGE 161
 QY 193 TCLPKALINLSNGENDITPVLLDIAERTGN-MREFINSPFRDIYRGOTALHAIERRCK 251
 Db 162 NLTAICLLQSGALHN-----LIARLINFPLINDICVSEYEGSPLHAIIVQDA 214
 QY 252 HYVELVAQADVAHAQARGRFQPKDE-----GGFYFGEPLIS 290
 Db 215 QFTSLRLRLGADLNQRCGAFCAADQKASRTSLHEHYELVLTNTNTYTGSMYFGEYPLS 274
 QY 291 LAACNQHPIVNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVTKVYDILL 350
 Db 275 FALCMGQHDLEFRLILA--KKANISADDTNGNTALH-LCVIHD--KK-DWL- 318
 QY 351 LKCARLEPDSNLEA--VINNDGLSPLMAAKTKIGIGIQTIRREVTBEDTRHLRK 405
 Db 319 -----DAVLBAAGNIRLANKONLTALTLAARLAK-----KTESIQHLE-- 356
 QY 406 FKDAAGPVYSIVDLSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRK 465
 Db 357 -----LMDGLLEQILDERKWA 372

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QY 466 FGAVSYINNVSYLCAMVIFLTAVYOPLEGTPPYRTVD----- 507
| : : : : :
Db 373 YGKALMMSLILGIFPFYCCFVCAVMLRPSATTEHLTRIGRIDDBESTNSTNYLQWHA 432
QY 508 -----YLRAGEVITLFT---GVLFFPTNIKDL-----PKKCKG 539
| : : : : :
Db 433 IDTOCHLMYASMPWYHGFRLGCEIMTIVMLFQILDFGDIRIGFOCKWENFLKAFPA 492
QY 540 VNSLFIDSGFOLLFYFYSVLVVSALYLAGIEAVLAV---MVFALVGMNNAFYTRG 595
| : : : : :
Db 493 --KLMFKKAF--LFITISIPCLAGSFH---EPFITINTMAIISILVQHFLYLYMA 544
QY 596 LKLTGTYSIMIOKILFKDLFRPLVYLLFMIGYASVSLNPCANMKVCNEDQNTCTVP 655
| : : : : :
Db 545 IFFVGPFVLMYVYITATDLVRPAMTYSIFLVGFSQGFYLFITSCE----- 589
QY 656 TTPSGCRDSTF-----STF-----LIDLPKLTIGMDL---EMLSTKYPVF 695
| : : : : :
Db 590 -----RDSIALKIDPMGSEFNNIMENPVALLRTFTIMTIGESVLYREMSACDNFMKRM 644
QY 696 IILVYIILTFVLLT--NMLIALMG---ETVGOVSKESKHIM 733
| : : : : :
Db 645 ICKLTFVIFETVYSILOFNLITAMTRTYETIFLRKMKRQW 687

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RESULT 10

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T24772
hypothetical protein t10b10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24772
R:Sim, M.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19934
A:Accession: T24772
A:status: preliminary; translated from GB/EMBL/DBJ
A:molecule type: DNA
A:Residues: 1-519 <WILL>
A:Cross-references: UNIPROT:Q22374; EMBL:Z72514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:TL
A:Experimental source: clone t10b10
C:Genetics:
A:Gene: CESP:T10B10.7
A:Map position: X
A:introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3

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Query Match 7.2%; Score 278; DB 2; Length 519;
Best Local Similarity 29.5%; Pred. No. 7.9e-12;
Matches 89; Conservative 36; Mismatches 115; Indels 62; Gaps 10;

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```

QY 216 IAEFTGNMEEFINSPP-RDIYR--GOTAIHAIERRCKHYVELVAQADVHAQARKP 272
| : : : : :
Db 161 VKQMTYRPFKIVNDIFLSEYYASVGLSPHQIIVNEDLEMYVFLCRKADVHQRCYGSF 220
QY 273 FQCKDE-----GGYFVGEGLPLSLAAGTQPHIVNYLTENPHKK 311
| : : : : :
Db 221 FCADDKASRTDLSLEHWDLVOSTKYTGQWGEYPLSPAACTNOVDCERLRA---MK 277
QY 312 ADMKRODSRGNTVLAHALVAIADNTRENTKFTQMYDLLLCKARLPDPSNLEAVLNDDG 371
| : : : : :
Db 278 ADPNMDDTNGNTYLH-----LTVIHDLPEFMPLAVELGANLH--VRNNLKI 321
QY 372 SPLMAAKTGKIGIFQHIIRREVTDERTRLSRKPKOMAYGPYSSLYLSDTGCER- 430
| : : : : :
Db 322 TPLALAAARKKIIYDLILE---CDMDI-----SMRYGPVCAKAYPLNDVDTINESD 370
QY 431 -----ASVLEIIVYNNKIEHRHMLAVEPINELRDKMRKRGAVSYINNVSYLCAMVF 485
| : : : : :
Db 371 GSINPNSVIANVYGVKVD--HLEFPDGLIEVLSESKWETGKKQLFMSLAGITVFLAVF 428
QY 486 TL 487
| : : : : :
Db 429 YL 430

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RESULT 11

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T19552
hypothetical protein C29B6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jul-2004
C:Accession: T19552
R:Johnson, R.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19141
A:Accession: T19552
A:status: preliminary; translated from GB/EMBL/DBJ
A:molecule type: DNA
A:Residues: 1-1188 <WILL>
A:Cross-references: UNIPROT:Q18297; EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C2
A:Experimental source: clone C29B6
C:Genetics:
A:Gene: CESP:C29B6.2
A:Map position: 4
A:introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

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Query Match 5.3%; Score 204.5; DB 2; Length 1188;
Best Local Similarity 20.3%; Pred. No. 4.1e-06;
Matches 152; Conservative 98; Mismatches 250; Indels 247; Gaps 33;

```

```

QY 124 RKIIERKQSPKAPAPQPPILKYFNRPIFDIYSKSGSTADLD-----GLPFLIT 175
| : : : : :
Db 418 RKKNKETERALKSPTRNTLRIVSDDVRYTVMVNRDQNTPMHIVASNGYLEMMQLQK 477
QY 176 HKKRLT---DEFPBSPGTCTLPKALINTL-----SNG 205
| : : : : :
Db 478 HNASITQVNEDEE-----TALHRAIAGVQLLEWDIRLLMDKDMGNSALHIAARG 529
QY 206 RNDTIPVLDIAERTGNMEEFINSPPRIYRGQTAIHAIRCKHYVELLVAQADVA 265
| : : : : :
Db 530 HDATTKVLLD-----NGADREAKNS-----YQ-KTFLQVAVDSGKLETCQRLVAKGAQIE 578
QY 266 AQ-----ARGFPQKQGGFYFGEGLPLSLAAGTQPHIVN 302
| : : : : :
Db 579 SSDDTYVLAHTAIFYGNEISIVRYFLAEGVTIDRDEEGKYAD-----IAC----- 624
QY 303 YLTENPHKKADMR-----ODSRGNTVLAHALVAIAD-----NTRENTKE---VTKMYDIL 349
| : : : : :
Db 625 ---ENDHK--DVAKAFLETDQMKMLIPCDVIPLDGHRPVMKRTPTTLTKPELA 679
QY 350 -----LAKCARLPDPSNLEAVLNDDGLSPLMAAKTGKIGIFQHIIR-REVTDEDTRLH 402
| : : : : :
Db 680 SFVMDKCIKSKBRTDSTQSAVYVNFPLDQTYMMRCVSDDGEGQLIGCKSAVDED----- 735
QY 403 SRKPKOMAYGPYSSLYLSDTGCBEASVLEIIVYN-----SKTENHMLAVEPINE 457
| : : : : :
Db 736 ---FKLEKDAQSAASYND-----RVYVHPLKIMADEKCH--LHNPILSK 776
QY 458 -LLRDKMRFGAVSFYINNVSYLCAMVIFLTAVYOPLEGTPPYRYRTVDYLRAGEV 516
| : : : : :
Db 777 ALIKYKMBLGRPMYFALFMYL--VFYSITQYVHTKA-----PVNNWNEESYDSE-- 828
QY 517 TLETGVLFPTNIKDLFMKKCPGVNSLFTD-----GSFOLLY----- 553
| : : : : :
Db 829 ---YFDEN-----ETCCPQINTTKEDVWKKIITQILVAQQLIVEGQLOKRRKAYL 875
QY 554 -----FYSVLYIV---SAAIYLAGIEAVLAVMVPALV---GMNALVFTGKLK 598
| : : : : :
Db 876 VMNENMIDCFIYSTALITYVDFEBCATSGVNRQNMOMIILALCTIFGMINTLHMIKKMR 935
QY 599 TGTYSIMIOKILFKDLFRPLVYLLFMIGYASVSLNPCANMKVCNEDQNTCTVP 658
| : : : : :
Db 936 FGLFVVMFVDIV-KTFRRFPFVFLFLIASSSFFVIL----- 972
QY 659 SCRDSFSTFLDLFKLTIGM-----GD-----LEMLSTKYPVFILVYTI 703
| : : : : :
Db 973 ---QNRPEFTIFWSPKTYVMIGEEFEFGIFHGEDTTHAEKMGPAHRAVACALFEFFC 1030

```


QY 704 ILTFLVLLNMLALMGETVGVSKSK 730
 Db 1031 IIMTILMLNMLVGLAVDIDIKGVQEKAE 1057

RESULT 12

trp3 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
 C:Accession: JCS807
 R:Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.
 Biochem. Biophys. Res. Commun. 240, 167-172, 1997
 A:Title: Expression and characterization of a trp1 homolog from rat.
 A:Reference number: JCS807; MUID:98042538; PMID:9367904
 A:Accession: JCS807
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-828 <PRE>
 A:Experimental source: brain
 A:Comment: This protein participates in store-operated Ca2+ entry into cells.
 C:Superfamily: TRPC3 protein

Query Match 4.9%; Score 188; DB 2; Length 828;
 Best Local Similarity 20.6%; Pred. No. 3.6e-05;
 Matches 137; Conservative 100; Mismatches 240; Indels 188; Gaps 31;

QY 210 IPVLIDIAERTGNMREFINSPRODIYRGOTAHIAIERCHYVELL-----VAQADV 264
 Db 52 IIVRAKMLBSRTLN--VNC-----VDYGNALQAVNEHLEVTLLKKENLARIGDA 105
 QY 265 -----HAQARGFQFP--KDEGFFYFGE-----LPLSLAA 293
 Db 106 LLMAISKGYRIVELIISHPALAQQTSLPLELRDD--FYDEGTGTFSPDITPIILAA 163
 QY 294 CTNOPIHYNYL-----TENPH--KKADMRD-----SRGNTLHALVAIADNT 335
 Db 164 HCHKEVVAHLLILKGRTERPHDYLCRCADCAEKQGLMTFSRSRINAYKASPGYLSLS 223
 QY 336 RENTFVTKMYDILLKCARLEPDSNLBAVANNODLSPLMAAKTKGIGF----- 386
 Db 224 SEDVPLTALLESNEIAKLA-----NIKEPKND--YRKLSPQCKDFVGVLDLCRDEEV 276
 QY 387 QHIIREVTDEDTN-----LSR-----KFKDWAYGVYSSLYDLSLPTCGEASV- 433
 Db 277 EAILNGDLESVEERHGHKASLSRYVLAIKVEKKFVANCOQQLITTYGMLSGELAIK 336
 QY 434 -LEILVNSKIENRHEMLAV-----EPINELLDRKKRFGAVSYINVSYLCAVVF 485
 Db 337 CLVVLVVALAL-----PFLAIGWIAIPCRLKILRSPMKFVAASFIL-----FLGLLVF 387
 QY 486 TLTAAYGPLEGTTPPYRYTVDYLRLAGEV--ITLFTGV-LFFPNIKDLPMKKCGVNSL 543
 Db 388 NASRPF--EGITLLENITVDYPRKQIFRYVTQTQWTEMLIMVWVGMMWSEC--KEL 441
 QY 544 FIDSGFOLLFYISYLVLS-----ALVYLAGIEAYLA----- 576
 Db 442 WLBPREFYQLMNVLDPLSIFIAFTARFLAFLCATGAQOQYVDSHQESLVEVTLPREV 501
 QY 577 -----VMQFALVGMNNAIYFTRGLKLTGYSIMIQKILFKDLF 615
 Db 502 QYFTYARDKWLPSDPOIISBGLVYAIAYVLSFSRIAYIIPANESFGPIQDISGRVY-KDIF 560
 QY 616 RFLVYLLFLMIGVASALVSLINPCANMKVCNEDQTCNVPTYPSCRDETFSTPLDLDFK 675
 Db 561 KFMVLFIVFLAFMIGMFLYSYVGARV--DPAFTV-----EESFKTLFWSIFG 609
 QY 676 LTIQAGDLBMLST-KYEVVFI-----ILVYIILFLVLLNMLALMGETVGVSKSK 729
 Db 610 LS-----EVTSVLKKDHFIEINIGYLVGIYVNTVVVLLNMLALMINSYQEIIBDS 663
 QY 730 KHIWK 734

Db 664 DVEMK 668

RESULT 13

calmodulin-binding protein trp1 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C:Accession: JH0588
 R:Phillips, A.M.; Bull, A.; Kelly, L.E.
 Neuron 8, 631-642, 1992
 A:Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with
 A:Reference number: JH0588; MUID:92232293; PMID:1314616
 A:Accession: JH0588
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1124 <PHI>
 A:Cross-references: UNIPROT:P48994; GB:M88185; NID:G463057; PID:G158715
 A:Experimental source: head
 C:Genetics:

A:Gene: trp1
 A:Cross-references: FlyBase:FBgn0005614
 C:Superfamily: TRPC3 protein

C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein
 F:341-362/Domain: transmembrane #status predicted <TM1>
 F:374-396/Domain: transmembrane #status predicted <TM2>
 F:462-479/Domain: transmembrane #status predicted <TM3>
 F:512-533/Domain: transmembrane #status predicted <TM4>
 F:549-572/Domain: transmembrane #status predicted <TM5>
 F:643-668/Domain: transmembrane #status predicted <TM6>
 F:710-727,809-825/Region: calmodulin binding #status predicted
 F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 3.8%; Score 145.5; DB 2; Length 1124;
 Best Local Similarity 19.3%; Pred. No. 0.057;
 Matches 141; Conservative 99; Mismatches 237; Indels 253; Gaps 34;

QY 189 STGKTCPEKALNLSNGNDITPVILD-----IARNG--NMREFINSPREDIYR--- 237
 Db 24 SVGGCCVPLGLPQ-----PILBEEKTLFAVERDMPVRRILOKALRHQININC 74
 QY 238 -----GOTAHIAIERCHYVELLVAQAD-----VHAQ 267
 Db 75 MDPLGRALTLAIENENLEWELLVWGVETKDALHAINAFVAVELLHHEBLYKE 134
 QY 268 ARGRFPQKDEGFFYFGEEL-PLSLACTNOPIHYNTEN-----PH----- 309
 Db 135 GEPYSQKVDINTAMFAPDITPMLAAHKNNFEILRLIDRGAAPVPHDRGCECVR 194
 QY 310 --KKADMRDQSRGN--TVLHALVAIADNTRENTK-----VTQM-----YDL 348
 Db 195 LTAEDSLRHSLSRNVITRALCSPSLICTSDPSSTATQLSWEIRNLALTQECKSEYMD 254
 QY 349 LILKCARLEPD-----SNLBAVLNNDGSLPLMAAKTKGIGFHIIIRREVTDEDT 400
 Db 255 LRQCQFPAVDLADQTRTSNELAITIYVD--PQMSVEPG-----DRM 295
 QY 401 HLSRKFQDMAYP--VYSSLYDL-----SSLD--TCGEASV--LEI 436
 Db 296 SLTRLVQAIISYQKKFVAHSNIQQLLSIWDGLPGFRKRISIVDKVICIAQVAVLFPVYC 355
 QY 437 LVVNSKIENRHEMLAVEPINELLDKMRKFGAVSYINVSYLCAMVFTLTAYYQPLEG 496
 Db 356 LIIYCARNCRIGQLMKRPF-----MKFLHASYSLLFFLIIIVS----- 395
 QY 497 TPYPYRYTVDYLRLAG-----EVITLFTGVLFEPFNIXDLF 533
 Db 396 -----QADDDFVRIFGTTRMKKELABQELRQGGTSPSKELIIVMVYIGVWEVEQEIF 450
 QY 534 MKKCGVNSL-----FIDSGFOLLFYISYLVLSAALYAGIE-----ATLAVVVF 580
 Db 451 ---AVGKSKSYLRNMNFIIDFLRNSLY--VSVMCLARAFYIQAATFIARDPQMAVYIPREK 505

QY 581 -----ALVLGMMNALYFTRGLKLTGTYSI-----MIQKILFK-----DLFRFLVYLFLMI 626
 Db 506 HDPFDQILAEGLFAAANFSAIKLVHLSINPLGLPQLSLGRMVIDIYKFFITIVLF 565
 QY 627 GYASALVSLINLNCAMKVCNEDQTNCTVPTP-----SCRDETFSTFLDLPK 675
 Db 566 AFACGLNQLIMYFAL-----EKSKCYV---LPGCADWGSBGDSCKMKRRFG-----NLPE 614
 QY 676 LT-----IGMDLEMLSTKYPVVF-IILVTVIILFVLILNMLLMGEIVGQ 724
 Db 615 SSQSLFWMSFGKVGDDFELSGITKSYTRFWMGLMFGSYVINIVILNLIAMNSYAM 674
 QY 725 VSKESKHIWK 734
 Db 675 IDEHSDTEWK 684

RESULT 14

TRPCL protein .. human
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
 C:Accession: I38361
 R.Wes, P.D.; Chevessich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
 Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
 A:Title: TRPCL, a human homolog of a Drosophila store-operated channel.
 A:Reference number: I38361; MUID:96003837; PMID:7568191
 A:Accession: I38361
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-810 <RES>
 A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
 C:Superfamily: TRPCL protein

Query Match 3.6%; Score 138.5; DB 2; Length 810;
 Best Local Similarity 18.1%; Pred. No. 0.11;

Matches 147; Conservative 126; Mismatches 315; Indels 223; Gaps 36;

QY 12 PCEVALPEDSGTSGEAFPLPSLANLPEGSDGSLSPADASRAGDGGPNIJMKF 71
 Db 3 PG---IPGRABAVGTHFPSSPGAWGSGSGS---GPVGAAPPSS----- 42
 QY 72 OGAFKRGVNPIDILESTLYESSVVPKAPMDSLFDGYRHHSSDNKRKKIIEKO 131
 Db 43 -----PGLPPSMAWMAALYPTSDLSGASSSL----- 70
 QY 132 POSKAPAPQPPILKVENRPIILFDIVSRGSTADLDGLPLTHKK---RLTDERPREP 188
 Db 71 PSSPSSSSPNEVWALK-----DVREYKEENTLNEKL-FLLACDKGYMVKLILEN 121
 QY 189 STGK---TCGP-----KALNLSNGRNDTIPVLLD-----IARTGNMREFFISPRDIY 235
 Db 122 SSQDLININCVDLGRAVITITENLDIQLLDLGGCKLMERIQNP---YSTMDV- 177
 QY 236 YRGQTAHIAIERCKHYVELLVAGADV---HA-QARGRFQPKDGGYFYFGEPLSL 291
 Db 178 ---AVIIIAAHNNYIITMLIKQDVSLPKPHAVACECTLCSAKKKKSLRHSRFLDI 233
 QY 292 AACTGNPHIVNYITENPHKKAMRRODSKGNVLAHLVAIAD-----NTRNTN 339
 Db 234 YRCLASPALIMTEEDP-----ILRAPELSADIKELSLIVEVERNDYEEL 278
 QY 340 KFTYKVDLLILKCALFPDSNLEAVLND-----GLSPYMAAAATGKI 383
 Db 279 ARQCKAFADILAQAR--NSRELEVLINHTSSDEPLDKGLBERNMLSLKIAIYN-- 334
 QY 384 GIFQHIIRREVTDETRHLSRKFKDMAYGVPVSYLDLSLDTGGERASVLEILVINSKI 443
 Db 335 -----QKEFVQSNN---COQFLANTYVW---FGOMSGYRRKPKCKIMTVLVGIF---- 377
 QY 444 ENRHEMLAVEPINELLRDKRRKGAIV-----SFYINNVSYLCAMITFTL-TAYYQPLEG 496

Db 378 -----WPVLSLYLIAEK-SQFGRITHTPPMKFIIHGASFTLLILLNLSLVYNEDK 430
 QY 497 TPPEYRTVTDYRLRAGAVITLFTSVLPFTNKKLFMKKCPGANSFLDGSFOLLIFY 556
 Db 431 NIMGPALRIDYL-----LILMITGMI--WSGIKLTWE---GLDD-FLIEBRNQLSPFM 479
 QY 557 SVLVIVSAALYIAG-----IAYLAVMY-----PALYLGMMNALYFTRGLK 598
 Db 480 NSLYIATFALKVVAANKKHFADRKMDAFHPTLVABGLFAFANVLSYLRLEFFMYTTSI 539
 QY 599 TGTYSIMIQKILFKDLFRFLVYLFLMIGYASALVSLINPCAMKVCNEDQTNCTVPTP 658
 Db 540 LGPLQISGQML-QDPGKFLGMLVLFSTFTGLQQLDXYGTSK---EQKDC-VGIFC 593
 QY 659 SCRDETFSTFLDLPFKLTIGWDEMLSTKYPVVF-----IILVTVI 703
 Db 594 EQGSDNTHPSIFGTCFAL-----FWYIFSLAHVALFVTRFSGBELQSGVAGVAYGTN 647
 QY 704 IITFVLLINMLIALMGEIVGVSKESKHIWK 734
 Db 648 VVVIVITLTKLIVAMLHKSFOLIANHEDKWK 678

RESULT 15

T00894
 hypothetical protein F21B7.8 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 R.Shinn, P.; Buehler, B.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con-
 eologis, A.; Ecker, J.R.
 Submitted to the EMBL Data Library, January 1998
 A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
 A:Reference number: Z14208
 A:Accession: T00894
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-616 <SH1>
 A:Cross-references: UNIPROT:Q9LR59; EMBL:AC002560; NID:g2618677; PID:g2809239; GSPDB:GNO
 C:Genetics:
 A:Gene: ATSP:F21B7.8
 A:Map position: 1
 A:introns: 229/1; 411/3

Query Match 3.6%; Score 137; DB 2; Length 616;
 Best Local Similarity 20.2%; Pred. No. 0.097;

Matches 123; Conservative 93; Mismatches 212; Indels 180; Gaps 30;

QY 161 GSTADLDGLPLPLTHKKRLTDEPREPSTGTCUPKA--LNLISGRNDTIPVLLDIAE 218
 Db 17 GSLSDEPDQWTF---KQKDESEIWNPAI--LCAVRAGDKVSLKRIINDVAVTORLVD 69
 QY 219 RTGN-----KREFTNSPP---RDIYRGQTAHIAIERCKHYVELLV--- 258
 Db 70 NQGNSTLHIAALGHVHIVFIISTPNNLQVNMLEGFTLLVAARAGSINIYELIVRF 129
 QY 259 -----AQCAD--VHAQARG-----FQPPDEGGYF----- 283
 Db 130 TESSSYDAFIARKSKNGDTALHAALKGKVEVAFCLVSVKHVDSFDKKNDEASPLYMAVE 189
 QY 284 ---FGEPLSLAACNTOPIHIVNLT-----NPHKKADM-----ROD 321
 Db 190 AGYHELVLMKLESSSSPSILASFSKSVTHAMKANRNDILGIVLRQDPGLIELRNEB 249
 QY 322 NYVLAHVALVADNTRENTKVTMYDILLKCARLFPDSNLEAVLNDGISPLMAAKTG 381
 Db 250 KTCLS--YGASMGVCYGIYRIIAEFD---KAA-----SSLGVADDDGFTPIHMAKSG 298
 QY 382 KIGIPQHIIR---REVTDETRH-----LSRKFDMAV-----GPVYSLVYDLS- 423
 Db 299 HVAIIRKFLKHCPSRELLINNOCONFHVAAIAGSKVVKYLLIKLDEGRMMNEODINGN 358
 QY 424 ---LDTGGEASVLEILVYNSKIENR---HEMLAVEPINELLRDKRRKGAVSFYINNV 476

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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:07:50 ; Search time 201 Seconds
(without alignments)
2124.020 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSSGPRAGPGVAELPG.....GVSKSKHIMKLGSRRL 742

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_02: *
2: uniprot_crembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3829	99.2	853	2	Q86YZ6
2	3829	99.2	871	2	Q8NDY7
3	3829	99.2	871	2	Q9HBCO
4	3829	99.2	871	2	Q9GQ92
5	3828	99.2	871	2	Q9HBAO
6	3695	95.8	871	2	Q9BPK8
7	3693	95.7	871	2	Q9BRZ8
8	3689	95.6	871	2	Q9EST6
9	3681	95.4	871	2	Q9EQZ4
10	3636	94.2	873	2	Q9BRZ7
11	3472	90.0	803	2	Q9BRZ7
12	3466	89.8	811	2	Q8NG64
13	3389	87.8	803	2	Q91XR5
14	3284	85.1	852	2	Q9DF53
15	1604.5	41.6	843	2	Q8QFN9
16	1603	41.6	839	2	Q8R5A3
17	1603	41.6	839	2	Q8R5A3
18	1598.5	41.4	839	2	AA513460
19	1580.5	41.0	838	2	Q8K1W1
20	1580	41.0	839	2	Q9UM57
21	1580	41.0	839	2	Q704Y3
22	1580	41.0	839	2	CAFO5661
23	1579.5	40.9	838	2	BAD20301
24	1579.5	40.4	839	2	C35433
25	1556.5	40.3	839	2	Q8NBT1
26	1555.5	40.3	839	2	Q8NBT2
27	1552.5	40.2	842	2	Q8RX08
28	1552.5	40.2	842	2	AA334458
29	1551.5	40.2	839	2	Q9H0G9
30	1551.5	40.2	839	2	Q9H304
31	1369	35.5	778	2	Q9JMS6

32	1324	34.3	761	2	Q9WUD2
33	1332	34.3	761	2	Q9QYH8
34	1332	34.3	762	2	Q9JMT8
35	1331	34.2	791	2	Q8K424
36	1316	34.1	790	2	Q8NFB2
37	1312	34.0	790	2	Q8NDW7
38	1309	33.9	765	2	Q8NBT9
39	1309	33.9	791	2	Q8NBT8
40	1304.5	33.8	756	2	Q6JGX2
41	1304.5	33.8	756	2	Q9WTR1
42	1304.5	33.8	756	2	Q9K771
43	1304.5	33.8	756	2	AA66752
44	1298.5	33.7	764	2	Q9Y5S1
45	1287	33.4	764	2	Q9Y670

ALIGNMENTS

RESULT 1

Q86YZ6 PRELIMINARY; PRT; 853 AA.

AC Q86YZ6; 01-JUN-2003 (TRMBLrel. 24, Created)
DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE Hypothetical protein TRPV-SV.
GN Name=TRPV-SV,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki S.;
RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Suzuki M.;
RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.

DR EMBL; AB100308; BAC55864.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005261; F:Cation channel activity; IEA.
DR GO; GO:0006812; P:Cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR008196; Cat_channel_Tryp.
DR InterPro; IPR008196; CytoK_IL1_Like.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; ANK_3.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1415; ANKYRIN.
DR PRINTS; PRO1768; TRPRECEPTOR.
DR PRINTS; PRO1769; VRLRECEPTOR.
DR SMART; SMO0248; ANK_3.
DR TIGRfams; TIGR00870; trp_1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR ANK repeat; Hypothetical protein; Ion transport; Ionic channel;
KW Transmembrane; Transport.
SQ SEQUENCE 853 AA; 96448 MW; EAA07196606AED20 CMC64;

Query Match 99.2%; Score 3829; DB 2; Length 853;

Best local Similarity 100.0%; Pred. No. 4e-233;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGVAELPGESGTPGGEAPPLSLANLTFPGEDGSLSPSPADASRPAPG 60
Db 1 MADSSGPRAGPGVAELPGESGTPGGEAPPLSLANLTFPGEDGSLSPSPADASRPAPG 60
Qy 61 GDGRPNLMKFGQAFRRGVNPNPDLLESTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 120

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Db 61 GGRNLMKFGQAFKGVNPIDILESTLYSSVPGPKAPMDSLEGYGTRHSSDN 120
Qy 121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLPILTHKKRL 180
Db 121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLPILTHKKRL 180
Qy 181 TDEEFPSTGKTCIPKALINLSNGRNDTIPVLDIAERTGNMREFINSPFDIYRGQT 240
Db 181 TDEEFPSTGKTCIPKALINLSNGRNDTIPVLDIAERTGNMREFINSPFDIYRGQT 240
Qy 241 ALHAIERRCKHYVELLVAGADVHAQAGRFQPPDEGGYFFGGLPLSLAATNQPHI 300
Db 241 ALHAIERRCKHYVELLVAGADVHAQAGRFQPPDEGGYFFGGLPLSLAATNQPHI 300
Qy 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
Qy 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDRHLNRKPKDMAYGVPYSSLYD 420
Db 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDRHLNRKPKDMAYGVPYSSLYD 420
Qy 421 LSLDTCGEBASVLEILVYNSKIENHMLAVEPINELADKMRKGAVSFYINVSYLIC 480
Db 421 LSLDTCGEBASVLEILVYNSKIENHMLAVEPINELADKMRKGAVSFYINVSYLIC 480
Qy 481 ANVIFLTAYYQPLGEGTPPYRTTYDYRLAGEVITLFTGVLPFTNIDLPKMKCPGV 540
Db 481 ANVIFLTAYYQPLGEGTPPYRTTYDYRLAGEVITLFTGVLPFTNIDLPKMKCPGV 540
Qy 541 NSLFDIGSPOLLYFYISVLYVSALYLAGIEAVLAVMVFALVGMNALYFRGLKLTG 600
Db 541 NSLFDIGSPOLLYFYISVLYVSALYLAGIEAVLAVMVFALVGMNALYFRGLKLTG 600
Qy 601 TYSIMQKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNEDQNCVPTPSC 660
Db 601 TYSIMQKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNEDQNCVPTPSC 660
Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLLNMLIALMGE 720
Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLLNMLIALMGE 720
Qy 721 TVGQVSKESKHWKLTQ 736
Db 721 TVGQVSKESKHWKLTQ 736

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RESULT 2

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Q8NDY7 PRELIMINARY; PRT; 871 AA.
ID 08NDY7;
AC 08NDY7;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Vanilloid receptor-like channel 2.
GN Name=VRL2;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
R1 SEQUENCE FROM N.A.
RX MEDLINE=2107054; PubMed=12077606;
RA Smith G.D., Gunthorpe M.J., Kelsell R.E., Hayes P.D., Reilly P.,
RA Racer P., Wright U.E., Jerman J.C., Walhin J.P., Ooi L., Egerton J.,
RA Charles K.J., Smart D., Randall A.D., Rand P., Davis U.B.,
RT TRPV3 is a temperature-sensitive vanilloid receptor-like protein.
RL Nature 418:186-190(2002).
EMBL: AJ296305; CAC82937.1; -.
DR Gene; HGNC:18063; TRPV4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.

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DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR008996; CytoK IL1 like.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRP channel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat, Ion transport, Ionic channel, Receptor, Transmembrane;
KW Transport.
SQ
SEQUENCE 871 AA; 98280 MW; C62056B86C5A6FB6 CRC64;

Query Match 99.2%; Score 3829; DB 2; Length 871;
Best Local Similarity 100.0%; Pred. No. 4.1e-233;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MADSSRGPRAGGEVAELPDESGTPGGAFLPSSIANLFEQDGLSPSPADASRPAQ 60
1 MADSSRGPRAGGEVAELPDESGTPGGAFLPSSIANLFEQDGLSPSPADASRPAQ 60
61 GGRNLMKFGQAFKGVNPIDILESTLYSSVPGPKAPMDSLEGYGTRHSSDN 120
61 GGRNLMKFGQAFKGVNPIDILESTLYSSVPGPKAPMDSLEGYGTRHSSDN 120
121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLPILTHKKRL 180
121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLPILTHKKRL 180
Qy 181 TDEEFPSTGKTCIPKALINLSNGRNDTIPVLDIAERTGNMREFINSPFDIYRGQT 240
Db 181 TDEEFPSTGKTCIPKALINLSNGRNDTIPVLDIAERTGNMREFINSPFDIYRGQT 240
Qy 241 ALHAIERRCKHYVELLVAGADVHAQAGRFQPPDEGGYFFGGLPLSLAATNQPHI 300
Db 241 ALHAIERRCKHYVELLVAGADVHAQAGRFQPPDEGGYFFGGLPLSLAATNQPHI 300
Qy 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
Qy 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDRHLNRKPKDMAYGVPYSSLYD 420
Db 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDRHLNRKPKDMAYGVPYSSLYD 420
Qy 421 LSLDTCGEBASVLEILVYNSKIENHMLAVEPINELADKMRKGAVSFYINVSYLIC 480
Db 421 LSLDTCGEBASVLEILVYNSKIENHMLAVEPINELADKMRKGAVSFYINVSYLIC 480
Qy 481 ANVIFLTAYYQPLGEGTPPYRTTYDYRLAGEVITLFTGVLPFTNIDLPKMKCPGV 540
Db 481 ANVIFLTAYYQPLGEGTPPYRTTYDYRLAGEVITLFTGVLPFTNIDLPKMKCPGV 540
Qy 541 NSLFDIGSPOLLYFYISVLYVSALYLAGIEAVLAVMVFALVGMNALYFRGLKLTG 600
Db 541 NSLFDIGSPOLLYFYISVLYVSALYLAGIEAVLAVMVFALVGMNALYFRGLKLTG 600
Qy 601 TYSIMQKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNEDQNCVPTPSC 660
Db 601 TYSIMQKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNEDQNCVPTPSC 660
Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLLNMLIALMGE 720
Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLLNMLIALMGE 720

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QY 721 TVGVSKSKHIMKIQ 736
Db 721 TVGVSKSKHIMKIQ 736

RESULT 3
ID Q9HBC0 PRELIMINARY; PRT; 871 AA.
AC Q9HBC0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE OTRPC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=renal cortex;
RX MEDLINE=20482174; PubMed=11025659;
RA Strickman R., Harteneck C., Numenmacher K., Schultz G., Plant T.D.;
RT "OTRPC4, a nonselective cation channel that confers sensitivity to
RT extracellular osmolarity";
RU Nat. Cell Biol. 2:695-702(2000).
DR EMBL; AF258465; AAG16127.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0015281; F:nonselective cation channel activity; NAS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripI.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR PRINTS; PRO1768; TRPVRECEPTOR.
DR PRINTS; PRO1769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; tlp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 871 AA; 98294 MW; C62056B86DEA6FB6 CRC64;

Query Match 99.2%; Score 3829; DB 2; Length 871;
Beet Local Similarity 100.0%; Pred. No. 4,1e-233;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSSEGRAPGGEVAAELPGDESGTGGGEAFPLSLIANLFGGFGSLSPSPADSRPAPG 60
Db 1 MADSSSEGRAPGGEVAAELPGDESGTGGGEAFPLSLIANLFGGFGSLSPSPADSRPAPG 60
QY 61 GDGSPNLRMKFQAGFRKGVNPIDLESTLYESSVVPKPKAPMDLSLFDYCTYRHSSDN 120
Db 61 GDGSPNLRMKFQAGFRKGVNPIDLESTLYESSVVPKPKAPMDLSLFDYCTYRHSSDN 120
QY 121 KRWKKTIEKOPQSPKAPAPPPPIIKVFNPIIFDIYSRGSYADLDGLPFLTHKKRL 180
Db 121 KRWKKTIEKOPQSPKAPAPPPPIIKVFNPIIFDIYSRGSYADLDGLPFLTHKKRL 180
QY 181 TDEEFREPSGTCTGLPALANLISNGRNDTIPVLDIARTQMMEEFINSPPRODIYYGQT 240
Db 181 TDEEFREPSGTCTGLPALANLISNGRNDTIPVLDIARTQMMEEFINSPPRODIYYGQT 240
QY 241 ALHAIARRCKHYVELLVAQADVAHQARGFPOPKDEGFGYFGEPLSLIACTNPHI 300
Db 241 ALHAIARRCKHYVELLVAQADVAHQARGFPOPKDEGFGYFGEPLSLIACTNPHI 300

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QY 301 VNYLTENPKKADMERQDSRGNTVLAVALADNTRENTKFTYKMYDILLKCARLPDS 360
Db 301 VNYLTENPKKADMERQDSRGNTVLAVALADNTRENTKFTYKMYDILLKCARLPDS 360
QY 361 NLEAVLNNDGLSPIMMAAKTKIGIPQHIIIRREVTDETRHLSRKPKDWAYGVPVSLYD 420
Db 361 NLEAVLNNDGLSPIMMAAKTKIGIPQHIIIRREVTDETRHLSRKPKDWAYGVPVSLYD 420
QY 421 LSLDTGGEASVLEIIVNSKIENRHEMLAEPINELRDQWRKGVNSFYINVSYL 480
Db 421 LSLDTGGEASVLEIIVNSKIENRHEMLAEPINELRDQWRKGVNSFYINVSYL 480
QY 481 AMVIFTLAAVYQPLEGTPPYPRITVDYRLAGEVITLFTGYLFPPTIKDLEPMKCPGV 540
Db 481 AMVIFTLAAVYQPLEGTPPYPRITVDYRLAGEVITLFTGYLFPPTIKDLEPMKCPGV 540
QY 541 NSLFTDGSFQIIFYTYSVIVISAAVYAGIAYLAVVFAVLGMNVALYTRTGKILTG 600
Db 541 NSLFTDGSFQIIFYTYSVIVISAAVYAGIAYLAVVFAVLGMNVALYTRTGKILTG 600
QY 601 TYSIMIOKILFQDLFRFLVYLLFMIGYASALVSLNPNANKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIOKILFQDLFRFLVYLLFMIGYASALVSLNPNANKVCNEDQNTCTVPTPSC 660
QY 661 RDSFTSTFLDLFLITIGMDLEMLSTKYVVFPIILVTYIILTFVLLNMLALMGE 720
Db 661 RDSFTSTFLDLFLITIGMDLEMLSTKYVVFPIILVTYIILTFVLLNMLALMGE 720
QY 721 TVGVSKSKHIMKIQ 736
Db 721 TVGVSKSKHIMKIQ 736

RESULT 4
ID Q96G92 PRELIMINARY; PRT; 871 AA.
AC Q96G92;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Vanilloid receptor like channel-2.
GN Name=VRL-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Ishibashi K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032427; BAB69040.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripI.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR PRINTS; PRO1768; TRPVRECEPTOR.
DR PRINTS; PRO1769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; tlp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
Transport.

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SQ SEQUENCE 871 AA; 98266 MW; C62056A401ECA8B6 CRC64;
 Query Match 99.2%; Score 3829; DB 2; Length 871;
 Best Local Similarity 100.0%; Pred. No. 4.1e-23;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSRGPRAGGEVAELPGDESGTPGGEAFPLSLANLFEGBDGLSPSPDASRPAPG 60
 DB 1 MADSSRGPRAGGEVAELPGDESGTPGGEAFPLSLANLFEGBDGLSPSPDASRPAPG 60
 QY 61 GGGPRLRMKFGAARFKGVNPIDILESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
 DB 61 GGGPRLRMKFGAARFKGVNPIDILESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
 QY 121 KWRKKIIEKOPSPAPAPPPPIIKVNRPLFDIVSRGSTADLDGLPLTHKKRL 180
 DB 121 KWRKKIIEKOPSPAPAPPPPIIKVNRPLFDIVSRGSTADLDGLPLTHKKRL 180
 QY 181 TDEFRPSTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPFDIYRGQT 240
 DB 181 TDEFRPSTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPFDIYRGQT 240
 QY 241 ALHIAIERCKHYVELVAQADVHAQARGFPQDEGGYFYFGEPLSLAATNOPIH 300
 DB 241 ALHIAIERCKHYVELVAQADVHAQARGFPQDEGGYFYFGEPLSLAATNOPIH 300
 QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTVKNYDILLKCARLPDS 360
 DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTVKNYDILLKCARLPDS 360
 QY 361 NLEAVLNNDGLSPDMAAATGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420
 DB 361 NLEAVLNNDGLSPDMAAATGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420
 QY 421 LSSLDTCGEASVLEILVYNSKIENHREMLAVEPINELLDKRRKGAVSFYINVSYL 480
 DB 421 LSSLDTCGEASVLEILVYNSKIENHREMLAVEPINELLDKRRKGAVSFYINVSYL 480
 QY 481 AMVIFTLTAYYOPLEGPPYRTYDYLRLAGEVITLFTGVLPFTNIDKLFMKKCPGV 540
 DB 481 AMVIFTLTAYYOPLEGPPYRTYDYLRLAGEVITLFTGVLPFTNIDKLFMKKCPGV 540
 QY 541 NSLFIIDSGFQLVFIYSVIVSALYLAGIEAYLAVMVFALVGMNNAVYTRGKL 600
 DB 541 NSLFIIDSGFQLVFIYSVIVSALYLAGIEAYLAVMVFALVGMNNAVYTRGKL 600
 QY 601 TYSIMIQKILFKDLFRPLVYLLFMIGYASALVSLNPGANMKVCNEDQNCVPTYPSC 660
 DB 601 TYSIMIQKILFKDLFRPLVYLLFMIGYASALVSLNPGANMKVCNEDQNCVPTYPSC 660
 QY 661 RDESTSTFLDLFKLTIKGDLEMLSTXYPVVFIILVYLLFTVLLNMLALMGE 720
 DB 661 RDESTSTFLDLFKLTIKGDLEMLSTXYPVVFIILVYLLFTVLLNMLALMGE 720
 QY 721 TVGQVSKESKHIWKLQ 736
 DB 721 TVGQVSKESKHIWKLQ 736

RESULT 5
 Q9HBA0 PRELIMINARY; PRT; 871 AA.
 AC Q9HBA0;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Vanilloid receptor-related osmotically activated channel.
 OS Name=VROAC;
 OS Homo sapiens (Human).
 OC Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiade; Homo.
 OC NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20531888; PubMed=11081638;
 RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
 RA Sali A., Hudepeth A.J., Friedman J.M., Heller S.;
 RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
 RT candidate vertebrate osmoreceptor.";
 RL Cell 103:525-535(2000).
 DR EMBL; AF263523; AAG28029.1; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:004872; F:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_Trlp.
 DR InterPro; IPR008996; CytoK_IL1_like.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR004729; TRPchannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR01768; TRPYRECEPTOR.
 DR PRINTS; PR01769; VRL2RECEPTOR.
 DR SMART; SM00248; ANK; 3.
 DR TIGRfam6; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50292; ANK_RBP_REGION; 1.
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KW Transport.

SQ SEQUENCE 871 AA; 98265 MW; A86FB6C9103C19 CRC64;
 Query Match 99.2%; Score 3828; DB 2; Length 871;
 Best Local Similarity 99.9%; Pred. No. 4.7e-23;
 Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSRGPRAGGEVAELPGDESGTPGGEAFPLSLANLFEGBDGLSPSPDASRPAPG 60
 DB 1 MADSSRGPRAGGEVAELPGDESGTPGGEAFPLSLANLFEGBDGLSPSPDASRPAPG 60
 QY 61 GGGPRLRMKFGAARFKGVNPIDILESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
 DB 61 GGGPRLRMKFGAARFKGVNPIDILESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN 120
 QY 121 KWRKKIIEKOPSPAPAPPPPIIKVNRPLFDIVSRGSTADLDGLPLTHKKRL 180
 DB 121 KWRKKIIEKOPSPAPAPPPPIIKVNRPLFDIVSRGSTADLDGLPLTHKKRL 180
 QY 181 TDEFRPSTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPFDIYRGQT 240
 DB 181 TDEFRPSTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPFDIYRGQT 240
 QY 241 ALHIAIERCKHYVELVAQADVHAQARGFPQDEGGYFYFGEPLSLAATNOPIH 300
 DB 241 ALHIAIERCKHYVELVAQADVHAQARGFPQDEGGYFYFGEPLSLAATNOPIH 300
 QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTVKNYDILLKCARLPDS 360
 DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTVKNYDILLKCARLPDS 360
 QY 361 NLEAVLNNDGLSPDMAAATGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420
 DB 361 NLEAVLNNDGLSPDMAAATGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420
 QY 421 LSSLDTCGEASVLEILVYNSKIENHREMLAVEPINELLDKRRKGAVSFYINVSYL 480
 DB 421 LSSLDTCGEASVLEILVYNSKIENHREMLAVEPINELLDKRRKGAVSFYINVSYL 480
 QY 481 AMVIFTLTAYYOPLEGPPYRTYDYLRLAGEVITLFTGVLPFTNIDKLFMKKCPGV 540
 DB 481 AMVIFTLTAYYOPLEGPPYRTYDYLRLAGEVITLFTGVLPFTNIDKLFMKKCPGV 540
 QY 541 NSLFIIDSGFQLVFIYSVIVSALYLAGIEAYLAVMVFALVGMNNAVYTRGKL 600


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Db      541 NSLFDGSPQLLYFTYSVAVISALVIGIEAYLAWVFWALVGLGMNALYFTRGKLTLG 600
Qy      601 TYSIMIQKILFKDLFRFLVLYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Db      601 TYSIMIQKILFKDLFRFLVLYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Qy      661 RDSERFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
Db      661 RDSERFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
Qy      721 TVGVSKSKSHIMKIQ 736
Db      721 TVGVSKSKSHIMKIQ 736

RESULT 6
Q9EPK8      PRELIMINARY; PRT; 871 AA.
AC      Q9EPK8;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE      01-MAR-2004 (TREMBLrel. 26, last annotation update)
DR      Transient receptor potential protein 12.
GN      Name=Trpv4; Synonyms=Trp12;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
EX      MEDLINE=20547522; PubMed=11094154;
RA      Wiesenbach U., Boedding M., Flockerzi V.,
RT      "Trp12, a novel Trp related protein from kidney.";
RL      FEBS Lett. 485:127-134(2000).
DR      EMBL; AJ296078; CAC20703.1; -.
DR      MGD; MGI:1926945; Trpv4.
DR      GO; GO:0005262; F:calcium channel activity; IDA.
DR      GO; GO:0005034; F:osmosensor activity; IDA.
DR      GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR      GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR      GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR      GO; GO:003103; P:vasopressin secretion; IMP.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR002111; Cat_channel_TrpL.
DR      InterPro; IPR008996; Cytok_IL1_like.
DR      InterPro; IPR005821; Ion_trans-
DR      InterPro; IPR004729; TRPChannel.
DR      InterPro; IPR008347; Vanil_receptor2.
DR      InterPro; IPR008348; Vanil_receptor2.
DR      Pfam; PF00023; ANK; 3.
DR      Pfam; PF00520; Ion_trans; 1.
DR      PRINTS; PR01768; TRPVRECEPTOR.
DR      PRINTS; PR01769; VRL2RECEPTOR.
DR      SMART; SM00248; ANK; 3.
DR      TIGRFAMs; TIGR00870; trp; 1.
DR      PROSITE; PS50088; ANK_REPEAT; 1.
DR      PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW      ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW      Transport.
SQ      SEQUENCE 871 AA; 98026 MW; 5BAC6E33F89CEA05 CRC64;

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Query Match      95.8%; Score 3695; DB 2; Length 871;
Best Local Similarity 95.7%; Pred. No. 1-2e-224;
Matches 704; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

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Qy      1 MAUSSBEPRAQPGVAVELPGDESGTPGGEAFPLISLANLFEFGDGLSPSPADASRPAPG 60
Db      1 MADGDGPRAPAGVAVPPGDESGTSGGEAFPLISLANLFEFGEGSSSLSPVDASRPAPG 60
Qy      61 GDGEPNLRMKFOGAFRGKGVNPRIDLLESTLYESSVVGPKKAPMDSLFDYCTYRHHSSDN 120

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Db      61 GDGEPNLRMKFOGAFRGKGVNPRIDLLESTLYESSVVGPKKAPMDSLFDYCTYRHHSSDN 120
Qy      121 KMRKKLIEKOPQSPKAPAPPPPPILKVNRRPILPDIVSRGSTADLDGLPFLTHKKKL 180
Db      121 KMRKKVVEKQSPAPAPPPPPILKVNRRPILPDIVSRGSTADLDGLPFLTHKKKL 180
Qy      181 TDEEFREBPGTKCLPKALNLSNGRNDIPLVLDIAETGNMREPIINSPPDIYRGQT 240
Db      181 TDEEFREBPGTKCLPKALNLSNGRNDIPLVLDIAETGNMREPIINSPPDIYRGQT 240
Qy      241 ALHIAIERCKHYVELVAQGDVHAQAGREFPOKDEGGYFPGELPLSLAAGTNPPI 300
Db      241 SLHIAIERCKHYVELVAQGDVHAQAGREFPOKDEGGYFPGELPLSLAAGTNPPI 300
Qy      301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKPYTKAYDILLKCARLPDS 360
Db      301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKPYTKAYDILLKCARLPDS 360
Qy      361 NLEAVIANDGSLPLMAAKTKIGIFQHIIRREVTDEPTRHLSRKFQMAVGPVYSSLYD 420
Db      361 NLEAVIANDGSLPLMAAKTKIGIFQHIIRREVTDEPTRHLSRKFQMAVGPVYSSLYD 420
Qy      421 LSSLDTCGEBAVLEILVYNSKIENRHEMLAVEPIINELLRDKMRKFGAVSFYINVSYLC 480
Db      421 LSSLDTCGEBAVLEILVYNSKIENRHEMLAVEPIINELLRDKMRKFGAVSFYINVSYLC 480
Qy      481 AMVIFTLAAYQPLEGTPPYPRPTVDYRLAGEVITLFTGLFFFTNKKDLFMKKCRPV 540
Db      481 AMVIFTLAAYQPLEGTPPYPRPTVDYRLAGEVITLFTGLFFFTNKKDLFMKKCRPV 540
Qy      541 NSLFDGSPQLLYFTYSVAVISALVIGIEAYLAWVFWALVGLGMNALYFTRGKLTLG 600
Db      541 NSLFDGSPQLLYFTYSVAVISALVIGIEAYLAWVFWALVGLGMNALYFTRGKLTLG 600
Qy      601 TYSIMIQKILFKDLFRFLVLYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Db      601 TYSIMIQKILFKDLFRFLVLYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTYPSC 660
Qy      661 RDSERFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
Db      661 RDSERFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
Qy      721 TVGVSKSKSHIMKIQ 736
Db      721 TVGVSKSKSHIMKIQ 736

RESULT 7
Q9ERZ8      PRELIMINARY; PRT; 871 AA.
AC      Q9ERZ8;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE      01-MAR-2004 (TREMBLrel. 26, last annotation update)
DR      Vanilloid receptor-related osmotically activated channel.
GN      Name=Vroac;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
EX      MEDLINE=20531888; PubMed=11081638;
RA      Liechte W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA      Sali A., Hudepeth A.J., Friedman J.M., Heller S.;
RT      "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT      candidate vertebrate osmoreceptor.";
RL      Cell 103:525-535(2000).
DR      EMBL; AF263521; AAG28027.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005261; F:calcium channel activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.

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DR GO:0006812; P: cation transport; IEA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002111; Cat_channel_TripL.
 DR InterPro: IPR008986; CytoC_IL1_Like.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR004729; TRPChannel.
 DR InterPro: IPR008347; Vanil_receptor.
 DR InterPro: IPR008348; Vanil_receptor2.
 DR Pfam: PF00023; Ank; 3.
 DR Pfam: PF00520; Ion_trans; 1.
 DR PRINTS: PR01768; TRPVRECEPTOR.
 DR SMART: SM00248; ANK; 3.
 DR TIGRFAMs: TIGR00870; tnp; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 1.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR ANK_repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KM Transport.
 SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;

Query Match 95.7%; Score 3693; DB 2; Length 871;

Best Local Similarity 95.5%; Pred. No. 1.6e-224;
 Matches 703; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

DR 1 MADSSRGPRAGGEVAELPDDESCTPGGEAFPLSLIANLFEGBDGSLSPPADASBPAGP 60
 1 MADPGGPRAPAEVAPEDDESCTGGEAFPLSLIANLFEGBDGSLSPPADASBPAGP 60
 QY 61 GNGRPNLRMKFGAARPKVNPIDLESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120
 QY 61 GNGRPNLRMKFGAARPKVNPIDLESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120
 DB 61 GNGRPNLRMKFGAARPKVNPIDLESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120
 QY 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 DB 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 QY 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 DB 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 QY 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 DB 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 QY 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 DB 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 QY 241 ALHIAIERCKHYVELLVAGADVHAQARFPQPDGGYFYGGLPLSLIACTNPHI 300
 DB 241 ALHIAIERCKHYVELLVAGADVHAQARFPQPDGGYFYGGLPLSLIACTNPHI 300
 QY 241 ALHIAIERCKHYVELLVAGADVHAQARFPQPDGGYFYGGLPLSLIACTNPHI 300
 DB 241 ALHIAIERCKHYVELLVAGADVHAQARFPQPDGGYFYGGLPLSLIACTNPHI 300
 QY 301 VNYLTENPKKADMRQDSRGNTVLHVALADNTRENTKVFYKMYDLILKCSRLEPDS 360
 DB 301 VNYLTENPKKADMRQDSRGNTVLHVALADNTRENTKVFYKMYDLILKCSRLEPDS 360
 QY 301 VNYLTENPKKADMRQDSRGNTVLHVALADNTRENTKVFYKMYDLILKCSRLEPDS 360
 DB 301 VNYLTENPKKADMRQDSRGNTVLHVALADNTRENTKVFYKMYDLILKCSRLEPDS 360
 QY 361 NLEAVLNNDGLSPILMAAATGKIGI FQHIIRREVTDEBTRHLSRKRDMAYGVYSSLYD 420
 DB 361 NLEAVLNNDGLSPILMAAATGKIGI FQHIIRREVTDEBTRHLSRKRDMAYGVYSSLYD 420
 QY 361 NLEAVLNNDGLSPILMAAATGKIGI FQHIIRREVTDEBTRHLSRKRDMAYGVYSSLYD 420
 DB 361 NLEAVLNNDGLSPILMAAATGKIGI FQHIIRREVTDEBTRHLSRKRDMAYGVYSSLYD 420
 QY 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPIINELRDKRKRGAVSFYINVSYL 480
 DB 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPIINELRDKRKRGAVSFYINVSYL 480
 QY 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPIINELRDKRKRGAVSFYINVSYL 480
 DB 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPIINELRDKRKRGAVSFYINVSYL 480
 QY 481 AMVIFLITAYQPLEGTPPYRYRTVLYRLAGEVITLFTGVLPFTNIRKDLFMKCCPGV 540
 DB 481 AMVIFLITAYQPLEGTPPYRYRTVLYRLAGEVITLFTGVLPFTNIRKDLFMKCCPGV 540
 QY 481 AMVIFLITAYQPLEGTPPYRYRTVLYRLAGEVITLFTGVLPFTNIRKDLFMKCCPGV 540
 DB 481 AMVIFLITAYQPLEGTPPYRYRTVLYRLAGEVITLFTGVLPFTNIRKDLFMKCCPGV 540
 QY 541 NSLFIDGSPQLLYFISVLAIVSAALYLAGIEAYLANVAVLVGMNNAIYFTRGLKLG 600
 DB 541 NSLFIDGSPQLLYFISVLAIVSAALYLAGIEAYLANVAVLVGMNNAIYFTRGLKLG 600
 QY 541 NSLFIDGSPQLLYFISVLAIVSAALYLAGIEAYLANVAVLVGMNNAIYFTRGLKLG 600
 DB 541 NSLFIDGSPQLLYFISVLAIVSAALYLAGIEAYLANVAVLVGMNNAIYFTRGLKLG 600
 QY 601 TYSIMOKILFKDLERFLVLYLLFMIGYASALVSLINPCANMKCNEDQNTCTVTPSC 660
 DB 601 TYSIMOKILFKDLERFLVLYLLFMIGYASALVSLINPCANMKCNEDQNTCTVTPSC 660
 QY 601 TYSIMOKILFKDLERFLVLYLLFMIGYASALVSLINPCANMKCNEDQNTCTVTPSC 660
 DB 601 TYSIMOKILFKDLERFLVLYLLFMIGYASALVSLINPCANMKCNEDQNTCTVTPSC 660
 QY 661 RDBESTETFLDLFKLITIGMDLEMLSSKXYPVFIILVLYIILFVLLNMLALMGE 720
 DB 661 RDBESTETFLDLFKLITIGMDLEMLSSKXYPVFIILVLYIILFVLLNMLALMGE 720
 QY 661 RDBESTETFLDLFKLITIGMDLEMLSSKXYPVFIILVLYIILFVLLNMLALMGE 720
 DB 661 RDBESTETFLDLFKLITIGMDLEMLSSKXYPVFIILVLYIILFVLLNMLALMGE 720
 QY 721 TVGQVSKSKHIMKQ 736

DB 721 TVGQVSKSKHIMKQ 736

RESULT 8
 Q9876 PRELIMINARY; PRT; 871 AA.

AC Q9876; AC
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE OTRPC4 cation channel.
 GN Name=Trpv4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=129/SvEv;
 RC MEDLINE=20482174; PubMed=11025659;
 RA Stroetmann R., Hatteneck C., Nunnemacher K., Schultz G., Plant T.D.;
 RT "OTRPC4, a nonselective cation channel that confers sensitivity to
 extracellular osmolarity.";
 RL Nat. Cell Biol. 2:695-702(2000).
 DR EMBL: AF208026; AAG17543.1; -;
 DR MGD; MGI:1926945; Trpv4.
 DR GO; GO:0005262; F:calcium channel activity; IDA.
 DR GO; GO:0005034; P:osmosensor activity; IDA.
 DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
 DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
 DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
 DR GO; GO:0030103; P:vasopressin secretion; IMP.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002111; Cat_channel_TripL.
 DR InterPro: IPR008996; CytoC_IL1_Like.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR004729; TRPChannel.
 DR InterPro: IPR008347; Vanil_receptor.
 DR InterPro: IPR008348; Vanil_receptor2.
 DR Pfam: PF00023; Ank; 3.
 DR Pfam: PF00520; Ion_trans; 1.
 DR PRINTS: PR01768; TRPVRECEPTOR.
 DR SMART: SM00248; ANK; 3.
 DR TIGRFAMs: TIGR00870; tnp; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 1.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR ANK_repeat; Ion transport; Ionic channel; Transmembrane; Transport.
 KM SEQUENCE 871 AA; 98069 MW; 2B228D554083F00A CRC64;

Query Match 95.6%; Score 3689; DB 2; Length 871;

Best Local Similarity 95.5%; Pred. No. 2.8e-224;
 Matches 703; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MADSSRGPRAGGEVAELPDDESCTPGGEAFPLSLIANLFEGBDGSLSPPADASBPAGP 60
 DB 1 MADPGGPRAPAEVAPEDDESCTGGEAFPLSLIANLFEGBDGSLSPPADASBPAGP 60
 QY 61 GNGRPNLRMKFGAARPKVNPIDLESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120
 DB 61 GNGRPNLRMKFGAARPKVNPIDLESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120
 QY 61 GNGRPNLRMKFGAARPKVNPIDLESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120
 DB 61 GNGRPNLRMKFGAARPKVNPIDLESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120
 QY 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 DB 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 QY 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 DB 121 KMRKKTIKOPSPKAPAPPPILKVFNRPIIPDIVSRGSTADIDGLPILLTHKKRL 180
 QY 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 DB 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 QY 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 DB 181 TDEEFPSPSTGKCLPKALINLSNGNDTI PVLLDIAERTGNMREPIINSPPFDIYYRGQT 240
 QY 241 ALHIAIERCKHYVELLVAGADVHAQARFPQPDGGYFYGGLPLSLIACTNPHI 300
 DB 241 ALHIAIERCKHYVELLVAGADVHAQARFPQPDGGYFYGGLPLSLIACTNPHI 300

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Db      241 SLHAIERCKHYVELVAQADVHAQARGFPQPKDEGYPYFGEPLSLAATNOPIH 300
Qy      301 VNYLTENPHKKAADMRQDSRGNTVLAHALVAADNTRENTKPYTKMYDLILKCARLPDS 360
Db      301 VNYLTENPHKKAADMRQDSRGNTVLAHALVAADNTRENTKPYTKMYDLILKCARLPDS 360
Qy      361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIREVTDEBTRHLSRKFQDMAYGVPVSSLYD 420
Db      361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIREVTDEBTRHLSRKFQDMAYGVPVSSLYD 420
Qy      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKGAVSFIYVSYLC 480
Db      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKGAVSFIYVSYLC 480
Qy      481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGVITLFTGVLPFTNFKDLFMKKGCV 540
Db      481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGVITLFTGVLPFTNFKDLFMKKGCV 540
Qy      541 NSLFDGSGFOLLFYISVLYVSAALYAGIBAYLAVWVFALVGMNALYFTRGKLTG 600
Db      541 NSLFDGSGFOLLFYISVLYVSAALYAGIBAYLAVWVFALVGMNALYFTRGKLTG 600
Qy      601 TYSIMIQILFKDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVPTPSC 660
Db      601 TYSIMIQILFKDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVPTPSC 660
Qy      661 RDSEFTSFLLDLFKLTIGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
Db      661 RDSEFTSFLLDLFKLTIGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
Qy      721 TVGVSKESKHIWKLQ 736
Db      721 TVGVSKESKHIWKLQ 736

RESULT 9
Q9EQZ4 PRELIMINARY; PRT; 871 AA.
AC Q9EQZ4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Ion channel.
GN Name=Trpv4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22692536; PubMed=12692122;
RA Suzuki M., Mizuno A., Kodaira K., Imai M.;
RT "Impaired pressure sensation in mice lacking TRPV4.";
RL J. Biol. Chem. 278:22664-22668(2003).
DR EMBL; AB021875; BAAB3731.2; -.
DR MGD; MGI:1926945; Trpv4.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047444; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004725; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion trans; 1.
DE PRINTS; PR01768; TRPVRECEPTOR.

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DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAM6; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 871 AA; 98060 MW; 3285A5E576D32D95 CRC64;

Query Match
Best Local Similarity 95.2%; Score 3681; DB 2; Length 871;
Matches 701; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy      1 MADSEGPAGGEAEALPGDESGTGGGAAPLSIANIFEGEDSLSPSPDASRPAGP 60
Db      1 MADPDGGRAPAGVAFEPGDESGTGGGAAPLSIANIFEGEDSLSPSPDASRPAGP 60
Qy      61 GDRPNLMPKQGAFAKGVPNPIDLSESTLYESSVYPGPKAPMDSLFDYGYRHHSSDN 120
Db      61 GDRPNLMPKQGAFAKGVPNPIDLSESTLYESSVYPGPKAPMDSLFDYGYRHHSPDN 120
Qy      121 KWRKRIIEKQPOSKAPAPQPPILKFNRPILFDYVRSSTADLDGLPFLTHKKRL 180
Db      121 KWRKRIIEKQPOSKAPAPQPPILKFNRPILFDYVRSSTADLDGLPFLTHKKRL 180
Qy      181 TDEEFREPSGTCTCPKALNLSNGRNDTIPVLIDIAERTGNMERFINSPPFDIYYRGQT 240
Db      181 TDEEFREPSGTCTCPKALNLSNGRNDTIPVLIDIAERTGNMERFINSPPFDIYYRGQT 240
Qy      241 ALHAIERCKHYVELVAQADVHAQARGFPQKDEGYPYFGEPLSLAATNOPIH 300
Db      241 SLHAIERCKHYVELVAQADVHAQARGFPQKDEGYPYFGEPLSLAATNOPIH 300
Qy      301 VNYLTENPHKKAADMRQDSRGNTVLAHALVAADNTRENTKPYTKMYDLILKCARLPDS 360
Db      301 VNYLTENPHKKAADMRQDSRGNTVLAHALVAADNTRENTKPYTKMYDLILKCARLPDS 360
Qy      361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIREVTDEBTRHLSRKFQDMAYGVPVSSLYD 420
Db      361 NLEAVLNNDGSLPLMAAKTGKIGFOHIIIREVTDEBTRHLSRKFQDMAYGVPVSSLYD 420
Qy      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKGAVSFIYVSYLC 480
Db      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKGAVSFIYVSYLC 480
Qy      481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGVITLFTGVLPFTNFKDLFMKKGCV 540
Db      481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGVITLFTGVLPFTNFKDLFMKKGCV 540
Qy      541 NSLFDGSGFOLLFYISVLYVSAALYAGIBAYLAVWVFALVGMNALYFTRGKLTG 600
Db      541 NSLFDGSGFOLLFYISVLYVSAALYAGIBAYLAVWVFALVGMNALYFTRGKLTG 600
Qy      601 TYSIMIQILFKDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVPTPSC 660
Db      601 TYSIMIQILFKDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVPTPSC 660
Qy      661 RDSEFTSFLLDLFKLTIGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
Db      661 RDSEFTSFLLDLFKLTIGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
Qy      721 TVGVSKESKHIWKLQ 736
Db      721 TVGVSKESKHIWKLQ 736

RESULT 10
Q9ERZ7 PRELIMINARY; PRT; 873 AA.
AC Q9ERZ7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.

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GN Name=Trpv4; Synonyms=Vroac;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=20531888; PubMed=11081638;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA Sait A., Hudspeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate vertebrate osmoreceptor.";
RL Cell 103:525-535(2000).
DR EMBL: AF263522; AAC28028.1; -.
DR MGI:1926945; Trpv4.
DR GO:GO:0005262; F:calcium channel activity; IDA.
DR GO:GO:0005034; F:osmosensor activity; IDA.
DR GO:GO:0042538; F:hyperosmotic salinity response; IMP.
DR GO:GO:0007231; F:osmosensory signaling pathway; IDA.
DR GO:GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO:GO:0030103; P:vasopressin secretion; IMP.
DR InterPro: IPR002110; Ank.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR008996; CytoK_IL1_like.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR008347; Vanil_receptor.
DR InterPro: IPR008348; Vanil_receptor2.
DR Pfam: PF00023; Ank; 3.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR01768; TRPVRECEPTOR.
DR PRINTS: PR01769; VRL2RECEPTOR.
DR SMART: SM00248; ANK; 3.
DR TIGRFAMs: TIGR00870; c1rp. 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ
SEQUENCE 873 AA; 98596 MW; 5DB87C92712B24BA CRC64;

Query Match          94.2%; Score 3636; DB 2; Length 873;
Best Local Similarity 94.4%; Pred. No. 6.3e-221;
Matches 697; Conservative 17; Mismatches 22; Indels 2; Gaps 2;

QY 1 MADSSGPPAAGPGEVAVLFDGDEGTGCGAFLPSSLANLFEEDGSLSPSPA-DASRPAG 59
DB 1 MADPGGPPAAPGEVAVLFDGDEGTGCGAFLPSSLANLFEEDGSLSPSPA-DASRPAG 60
QY 60 PGDGRPNLNMKF-OGAFKRGVNPIDLLSTLYESSVVGPKKAPMDSLFDYGYRHSS 118
DB 61 PGDGRPNLNMKRFKRSAPKGVNPIDLLSTLYESSVVGPKKAPMDSLFDYGYRHSS 120
QY 119 DNGKWKRTIEKQPGSPKAPAPPPPIIKVFNPPIIFDIYSRGSSTADLGLPLILTHKK 178
DB 121 DNGKWKRTIEKQPGSPKAPAPPPPIIKVFNPPIIFDIYSRGSSTADLGLPLILTHKK 180
QY 179 RLTFDEFPRESTGKTCLPKALNLSNGRNDTIVLLDIARTGNMSEFINSFPRDIYRG 238
DB 181 RLTFDEFPRESTGKTCLPKALNLSNGRNDTIVLLDIARTGNMSEFINSFPRDIYRG 240
QY 239 QFALHAIERRCGHVYELVAQADVAQAQGRFPQPKDGGYFYFGELPLSLAACPNO 298
DB 241 QFSLHAIERRCGHVYELVAQADVAQAQGRFPQPKDGGYFYFGELPLSLAACPNO 300
QY 299 HINVTITENHKKADMRQDSRGNTVLAHVAIADNTRNTKYTKYDILLKCARLP 358
DB 301 HINVTITENHKKADMRQDSRGNTVLAHVAIADNTRNTKYTKYDILLKCARLP 360
QY 359 DSNLEAVLNDGSLPLMAKTKTGIFGHIIRREVTDENTRLSRFKDWAYGPPVSSL 418
DB 361 DSNLEAVLNDGSLPLMAKTKTGIFGHIIRREVTDENTRLSRFKDWAYGPPVSSL 420

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QY 419 YDLSLDTGGEASVLEILVYNSKIENHMLAVEPINELLIDPKRKRGANSFYINVSY 478
DB 421 YDLSLDTGGEASVLEILVYNSKIENHMLAVEPINELLIDPKRKRGANSFYINVSY 480
QY 479 LCAWVIFLTVAYOPLDETPPYPTTVDYRLAGEVTLFTGVLFPPFNKDLFMKPCP 538
DB 481 LCAWVIFLTVAYOPLDETPPYPTTVDYRLAGEVTLFTGVLFPPFNKDLFMKPCP 540
QY 539 GVNSLFDIGSFQLLYFIYSVIVSAALYLAGIENAVLAWVFALVGMNALYFTRGLKL 598
DB 541 GVNSLFDIGSFQLLYFIYSVIVSAALYLAGIENAVLAWVFALVGMNALYFTRGLKL 600
QY 599 TGTYSIMIQKTLFKDLFRFLVYLLEPMIGYASALVSLNPPCANMVCNEDQNCVPTYP 658
DB 601 TGTYSIMIQKTLFKDLFRFLVYLLEPMIGYASALVSLNPPCANMVCNEDQNCVPTYP 660
QY 659 SCRDSEFTFLDLFKLTIGMGDEMLSTKYPVVFILLVYIILTFVILLNMLIALM 718
DB 661 ACRDSEFTSALFLDLFKLTIGMGDEMLSSAKYPVVFILLVYIILTFVILLNMLIALM 720
QY 719 GETVQGVSKESKHIMKIQ 736
DB 721 GETVQGVSKESKHIMKIQ 738

RESULT 11
Q96RS7 PRELIMINARY; PRT; 803 AA.
ID Q96RS7;
AC Q96RS7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN Name=VRL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Deret C., Schaefer M.K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RX EMBL: AF279673; AKK69487.1; -.
DR GO:GO:0016021; C:integral to membrane; IEA.
DR GO:GO:0005261; F:calcium channel activity; IEA.
DR GO:GO:004872; F:receptor activity; IEA.
DR GO:GO:006812; P:calcium transport; IEA.
DR InterPro: IPR002110; Ank.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR008996; CytoK_IL1_like.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR004729; TrpChannel.
DR InterPro: IPR008347; Vanil_receptor.
DR InterPro: IPR008348; Vanil_receptor2.
DR Pfam: PF00023; Ank; 3.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR01768; TRPVRECEPTOR.
DR PRINTS: PR01769; VRL2RECEPTOR.
DR SMART: SM00248; ANK; 3.
DR TIGRFAMs: TIGR00870; c1rp. 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ
SEQUENCE 803 AA; 91635 MW; AB329C595B325784 CRC64;

Query Match          90.0%; Score 3472; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 1.3e-210; Indels 0; Gaps 0;
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 MKFGAIFRKGVNPIDLLSTLYESSVVGPKKAPMDSLFDYGYTYRHSSDNGKWKRTII 128

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Db      1 MFGQAFKRGVNPIDLESTLYESSVGPCKAPMDSLFDYGTGRHSSDMKRRKII 60
Qy      129 EKQPOS PKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPFLTHKKRLTDEFRP 188
Db      61 EKQPOS PKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPFLTHKKRLTDEFRP 120
Qy      189 STGKTCPLKALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIYRGQALHAIALER 248
Db      121 STGKTCPLKALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIYRGQALHAIALER 180
Qy      249 RCKHYVELLVAGQAVHAQARGFPQPKDEGGYFFGELPLSLAATNQPPIVNTLTPN 308
Db      181 RCKHYVELLVAGQAVHAQARGFPQPKDEGGYFFGELPLSLAATNQPPIVNTLTPN 240
Qy      309 HKKADMRRODSRGNTVLAHVLAADNTRENTKFTVMYDILLKCARLPDSNLEAVLNN 368
Db      241 HKKADMRRODSRGNTVLAHVLAADNTRENTKFTVMYDILLKCARLPDSNLEAVLNN 300
Qy      369 DGLSPILMAAATGKTGIFQHIIRREVTDERTRLSRKFKDMAVGPVSSLYDLSLDTG 428
Db      301 DGLSPILMAAATGKTGIFQHIIRREVTDERTRLSRKFKDMAVGPVSSLYDLSLDTG 360
Qy      429 EASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYLCAWYIFLIT 488
Db      361 EASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYLCAWYIFLIT 420
Qy      489 AAYPLSGTPPYRYRTTYDYLRLAGEVITLFTGVLPFTNIDLEFMKCPGVNSLFDIGS 548
Db      421 AAYPLSGTPPYRYRTTYDYLRLAGEVITLFTGVLPFTNIDLEFMKCPGVNSLFDIGS 480
Qy      549 FQLYFYISVLYVSALYLAGIEAYLAVMFPALVGMNNAALYFTRGKLTGTYSIMQX 608
Db      481 FQLYFYISVLYVSALYLAGIEAYLAVMFPALVGMNNAALYFTRGKLTGTYSIMQX 540
Qy      609 ILFDLRFPLLYVLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSCROSETST 668
Db      541 ILFDLRFPLLYVLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSCROSETST 600
Qy      669 FLDDLKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLINMLALMGETVGOVSK 728
Db      601 FLDDLKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLINMLALMGETVGOVSK 660
Qy      729 SKHIMKIQ 736
Db      661 SKHIMKIQ 668

RESULT 12
Q8NG64 PRELIMINARY; PRT; 811 AA.
AC Q8NG64;
DT 01-OCT-2002 (Tremblere, 22, Created)
DT 01-OCT-2002 (Tremblere, 22, last sequence update)
DT 01-MAR-2004 (Tremblere, 26, last annotation update)
DS ORPCCbeta cation channel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose endoderm;
RA Xu F., Satoh E., Iijima T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073669; BAC06573.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR008996; Cytok rll_1ike.
DR InterPro; IPR005821; Ion_trans.

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DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKRIN.
DR PRINTS; PR01768; TRYPRECEPTOR.
DR SMART; SM00248; ANK; 3.
DR SMART; SM00248; ANK; 3.
DR PROSITE; PS00088; ANK_REPEAT; 1.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR ANK Repeat; Ion transport; Ionic channel; Transmembrane; Transport.
DR ANK Repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SEQUENCE 811 AA; 91220 MW; 38470D0FD07830781 CRC64;

Query Match      89.8%; Score 3466; DB 2; Length 811;
Best Local Similarity 91.6%; Pred. No. 3,1e-210; Indels 60; Gaps 1;
Matches 674; Conservative 0; Mismatches 2;

Qy      1 MADSEGPRAAGPEVAVLPGDESGTPGGEAPPLSLANLPEGEDSLSPSPADASRPAGP 60
Db      1 MADSEGPRAAGPEVAVLPGDESGTPGGEAPPLSLANLPEGEDSLSPSPADASRPAGP 60
Qy      61 GDGRPNLPMKQAFKRGVNPIDLESTLYESSVGPCKAPMDSLFDYGTGRHSSDN 120
Db      61 GDGRPNLPMKQAFKRGVNPIDLESTLYESSVGPCKAPMDSLFDYGTGRHSSDN 120
Qy      121 KRWKKIIEKQPOS PKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPFLTHKKRL 180
Db      121 KRWKKIIEKQPOS PKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPFLTHKKRL 180
Qy      181 TDEEFREPSGTGTCPLKALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIYRGQ 240
Db      181 TDEEFREPSGTGTCPLKALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIYRGQ 240
Qy      241 ALHAIARRCHYVELLVAGQAVHAQARGFPQPKDEGGYFFGELPLSLAATNQPPI 300
Db      241 ALHAIARRCHYVELLVAGQAVHAQARGFPQPKDEGGYFFGELPLSLAATNQPPI 300
Qy      301 VNYLTENPHKKADMRRODSRGNTVLAHVLAADNTRENTKFTVMYDILLKCARLPDS 360
Db      301 VNYLTENPHKKADMRRODSRGNTVLAHVLAADNTRENTKFTVMYDILLKCARLPDS 360
Qy      361 NLEAVLNNDGLSPILMAAATGKTGIFQHIIRREVTDERTRLSRKFKDMAVGPVSSLYD 420
Db      361 NLEAVLNNDGLSPILMAAATGKTGIFQHIIRREVTDERTRLSRKFKDMAVGPVSSLYD 420
Qy      421 LSLDTCGERASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYL 480
Db      421 LSLDTCGERASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYL 480
Qy      481 AMVIFTLTAYYOPLEGTPPYRYRTTYDYLRLAGEVITLFTGVLPFTNIDLEFMKCPGV 540
Db      421 AMVIFTLTAYYOPLEGTPPYRYRTTYDYLRLAGEVITLFTGVLPFTNIDLEFMKCPGV 480
Qy      541 NSLFDIGSPQLYFYISVLYVSALYLAGIEAYLAVMFPALVGMNNAALYFTRGKLTG 600
Db      481 NSLFDIGSPQLYFYISVLYVSALYLAGIEAYLAVMFPALVGMNNAALYFTRGKLTG 540
Qy      601 TYSIMOKILFKDLRFPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
Db      541 TYSIMOKILFKDLRFPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 600
Qy      661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLINMLALMGE 720
Db      601 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLINMLALMGE 660
Qy      721 TVGQVSKESGHIMKIQ 736
Db      661 TVGQVSKESGHIMKIQ 676

RESULT 13
Q91XR5 PRELIMINARY; PRT; 803 AA.
ID Q91XR5

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AC 091XR5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Vanilloid receptor-like protein 2.
 GN Name=Trpv4; Synonyms=Vrl2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Derst C., Schafer M.K.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DB EMBL; AF279672; AK69486.1; -
 DR MGI; MGI:1926945; Trpv4.
 DR GO; GO:0005262; F:calcium channel activity; IEA.
 DR GO; GO:0005034; F:osmosensor activity; IEA.
 DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
 DR GO; GO:0007231; P:osmosensory signaling pathway; IEA.
 DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
 DR GO; GO:0030103; P:vasopressin secretion; IMP.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_Trlp.
 DR InterPro; IPR008996; CytoK_IL1_like.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PRO1415; ANKTRIN.
 DR PRINTS; PRO1768; TRPVRECEPTOR.
 DR PRINTS; PRO1769; VRL2RECEPTOR.
 DR SMART; SM00248; ANK; 3.
 DR TIGRFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_RRP_REGION; 1.
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KM Transport.
 SQ SEQUENCE 803 AA; 91438 MW; 79A5BD9323300029 CRC64;
 Query Match 87.8%; Score 3389; DB 2; Length 803;
 Best Local Similarity 96.6%; Pred. No. 2,2e-205;
 Matches 645; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

DB 361 EEVSVEILVYNSKIENRHEMLAVEPINELIRDKRRKGAVSFYINVSICAMVITLT 420
 QY 489 AAYQPLRGTPPYPRRTVVDYLRLAGEVITLFTGYLFFPTNIKDI PMKCPGVNSLFDGS 548
 DB 421 AAYQPLRGTPPYPRRTVVDYLRLAGEVITLFTGYLFFPTSIKDIPTKCPGVNSLFDGS 480
 QY 549 FQLYPIYSVLVYSALYIAGIAYAVLVAVVAFALVGMNMLYTRGKLTGYSIMIQK 608
 DB 481 FQLYPIYSVLVYSALYIAGIAYAVLVAVVAFALVGMNMLYTRGKLTGYSIMIQK 540
 QY 609 ILFDLFRFLVYLILFMIGYASALVSLNPCANNKVCNEDQNTCTVPTYPSCRDSEFST 668
 DB 541 ILFDLFRFLVYLILFMIGYASALVSLNPCANNKVCNEDQNTCTVPTYPSCRDSEFST 600
 QY 669 FLDDLFKLTIGMDLMLSTKYPVVFILVYIILTFVLLNMLTLMGETVQVSK 728
 DB 601 FLDDLFKLTIGMDLMLSTKYPVVFILVYIILTFVLLNMLTLMGETVQVSK 660
 QY 729 SKIHWKIQ 736
 DB 661 SKIHWKIQ 668
 RESULT 14
 ID Q9DF53 PRELIMINARY; PRT; 852 AA.
 AC Q9DF53;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Vanilloid receptor-related osmotically activated channel protein.
 GN Name=VR-ORC;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxId=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cochlea;
 RX MEDLINE=20531888; PubMed=11081638;
 RA Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,
 Hudspeth A.J., Friedman J.M., Heller S.;
 DE "Vanilloid receptor-related osmotically activated channel (VR-ORC), a
 candidate vertebrate osmoreceptor.";
 RT Cell 103:525-535(2000).
 RL EMBL; AF261883; AAG28026.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005262; C:integral channel activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006812; F:cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_Trlp.
 DR InterPro; IPR008996; CytoK_IL1_like.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR002016; Peroxidase.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PRO1415; ANKTRIN.
 DR PRINTS; PRO1768; TRPVRECEPTOR.
 DR PRINTS; PRO1769; VRL2RECEPTOR.
 DR SMART; SM00248; ANK; 3.
 DR TIGRFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_RRP_REGION; 1.
 DR PROSITE; PS500436; PEROXIDASE_2; UNKNOWN_1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KM Transport.

SQ SEQUENCE 852 AA; 96197 MW; E85365D3FADD08C1 CRC64;
 Query Match 85.1%; Score 3284; DB 2; Length 852;
 Best Local Similarity 86.5%; Pred. No. 1e-198;
 Matches 624; Conservative 43; Mismatches 50; Indels 4; Gaps 2;

QY 17 ELFGDESTPGGEAFPLSSLANLPFGEDGSLSPSPADASR-PAGDGRPNLRMKFGQAF 75
 DB 5 EDPKADGVLDGDDSPFLSSLANLPFEVD---TPSPAPSRGPPGAGDKQMLRMKFGHAF 61
 QY 76 RKGVPNPIDLLESTLYESSVYVGPKKAPMDSLFDVGTGRHSSDNKRKKIIEKQPS 135
 DB 62 RKGPKPMELLESSTLYESSVYVAPKKAPMDSLFDVGTGRHSPSEKRRRRVVEKPVAGT 121
 QY 136 KAPAPQPPPLIKVFNRPILFDIVSRGSTRADLGLPLFLTHKKLTLDEFPSTGKTCL 195
 DB 122 KGPAPNPPLVLFVFNRPILFDIVSRGSDGLBGLSLFLTHKKLTLDEFPSTGKTCL 181
 QY 196 PKALLNLSGNGNDITPVLDAERTGNMRETFNSPFDIYRGOTAHIAIERCKAYE 255
 DB 182 PKALLNLSGNGNDITPVLDAERTGNMRETFNSPFDIYRGOTAHIAIERCKAYE 241
 QY 256 LIVAQADVHAQAGRFPPQDEGGYFPGELPLSLAAGTNOPIHIVYLTENPKKADMR 315
 DB 242 LIVAQADVHAQAGRFPPQDEGGYFPGELPLSLAAGTNOPIHIVYLTENPKKADMR 301
 QY 316 RQDSRGNTVLAVALADNTRENTKFTVYKMYDLILKCARLFPNSLEAVLNDSPLM 375
 DB 302 RQDSRGNTVLAVALADNTRENTKFTVYKMYDLILKCARLFPNSLEAVLNDSPLM 361
 QY 376 MAATGKIGIFQHIIRREAVTDETRHLSRKKQMAVGPVYSLYDSSLDTGGEASVLE 435
 DB 362 MAATGKIGIFQHIIRREAVTDETRHLSRKKQMAVGPVYSLYDSSLDTGGEASVLE 421
 QY 436 ILVNSKLENRHEMLAEPINELRLDKWRKGAVSFTINVSYSICANVIFLTATYQPLE 495
 DB 422 ILVNSKLENRHEMLAEPINELRLDKWRKGAVSFTINVSYSICANVIFLTATYQPLE 481
 QY 496 GTPPYPTVTVLRLAGEVITLFTGVLPFTNIKDLFMKKCPGVNSLFDIGSPQLYFI 555
 DB 482 GTPPYPTVTVLRLAGEVITLFTGVLPFTNIKDLFMKKCPGVNSLFDIGSPQLYFI 541
 QY 556 YSVLVYSAALYAGTAYLAWVFALVLCWMAALYTRGKLTGYYSIMIOKTLFIDL 615
 DB 542 YSVLVYSAALYAGTAYLAWVFALVLCWMAALYTRGKLTGYYSIMIOKTLFIDL 601
 QY 616 RFLVYLLFMIGYASALVSLNPPCANVCNBDQNCVPTYPSCRDSEPFELDLFK 675
 DB 602 RFLVYLLFMIGYASALVSLNPPCANVCNBDQNCVPTYPSCRDSEPFELDLFK 661
 QY 676 LTIQMDLEMLSTKYPVVFILLYVYIILTFVLLNMLTALMGETVGOVSKSKHIMKL 735
 DB 662 LTIQMDLEMLSTKYPVVFILLYVYIILTFVLLNMLTALMGETVGOVSKSKHIMKL 721
 QY 736 Q 736
 DB 722 Q 722

RESULT 15
 OBOEN9 PRELIMINARY; PRT; 843 AA.
 ID OBOEN9
 AC OBOEN9
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DB Vanilloid receptor-like protein.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Dorsal root ganglia;
 RX MEDLINE=21842900; PubMed=11853675;
 RA Jordt S.E., Julius D.,
 RT "Molecular basis for species-specific sensitivity to 'hot' chill
 peptides";
 RL Cell 108:421-430(2002).
 DR EMBL; AY072909; AAL78069.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat channel_TripL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; ANK; 3.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR01768; TRPRECEPTOR.
 DR SMART; SM00248; ANK; 4.
 DR TIGRFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KM ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KM Transport.
 SQ SEQUENCE 843 AA; 96520 MW; ABB3592C9DC179C8 CRC64;

Query Match 41.6%; Score 1604.5; DB 2; Length 843;
 Best Local Similarity 47.5%; Pred. No. 1.2e-97;
 Matches 343; Conservative 126; Mismatches 164; Indels 67; Gaps 18;

QY 41 EGEDSLSPSPADASRPAGDGRPNLRMKFGAQRKGVNPIDLLESTLY--ESSVYV 98
 DB 27 DGEDSL--ETAD-----GTYRHHSSDNKRKKIIEKQPS--OSPPAPAPQPPIL 146
 QY 99 ---PKKAPMDSLPDY-----GTYRHHSSDNKRKKIIEKQPS--OSPPAPAPQPPIL 146
 DB 65 DCDKDMAPMDSFYOMDHMAPSVYKFFANNEGRKHLTSDSTTGSEKRA-----F 116
 QY 147 KVENRPILFDIVSRGSTRADLGLPLFLTHKKLTLDEFPSTGKTCLPKALLNLSNGR 206
 DB 117 KFYDRRIIFDAVARGSKDLDLLVYLRKTLKHLTDEFPSTGKTCLKAMLNLDGK 176
 QY 207 NDTIPVLDAERTGNMRETFNSPFDIYRGOTAHIAIERCKAYVELLVAQADVHA 266
 DB 177 NDTIPVLDAERTGNMRETFNSPFDIYRGOTAHIAIERCKAYVELLVAQADVHA 236
 QY 267 QARGRFQPP--KDGSGYFPEELPLSLAAGTNOPIHIVYLTENPKKADMRQDSRGNTV 325
 DB 237 QARGRFQPP--KDGSGYFPEELPLSLAAGTNOPIHIVYLTENPKKADMRQDSRGNTV 295
 QY 326 HALVALADNTRENTKFTVYKMYDLILKCARLFPNSLEAVLNDSPLMMAATGKIGI 385
 DB 296 HTLVELADNTKDMTKFTVYKMYDLILKCARLFPNSLEAVLNDSPLMMAATGKIGI 355
 QY 386 FQHIIRREAVTDETRHLSRKKQMAVGPVYSLYDSSLDTGGEASVLEILVNSKLEN 445
 DB 356 FAYILREIKDPCRHLSRKKQMAVGPVYSLYDSSLDTGGEASVLEILVNSKLEN 414
 QY 446 RHEMLAVEPINEELRLDKWRKGAVSFTINVSYSICANVIFLTATYQPLE--GTPPY- 502
 DB 415 RHEMLAVEPINEELRLDKWRKGAVSFTINVSYSICANVIFLTATYQPLE--GTPPY- 474
 QY 503 RTVDYLRLAGEVITLFTGVLPFTNIKDLFMKKCPGVNSLFDIGSPQLYFYYSVAVI 562
 DB 475 HSGVGFRTVLTGLSVAGLYFFFRIGQ--YFVGRRSIKTLVYDYSSEVLFVHSHLLLS 533
 QY 563 SAALYLAGIEAYLAWVFALVLCWMAALYTRGKLTGYYSIMIOKTLFIDLFRPLLYVL 622

```

Db      534  SVVLYFCGQELIYASWVFSIALGNANMLYTRGFCQMGIVSMIAKMLIRDLCRMFVYL 593
QY      623  LFMIGYASALVSLINPCANMKVCNEDQ-TNCTVPTYBSCRDESEST-----FLDLE 674
Db      594  VFLIGFSTAVVTLIED-----DNEGQDTNS--FYACSHTKRGRTSYNSLYTCLLEF 645
QY      675  KLITGMGDLLEMLSSIKYPVFIILVYIILTFVILLMLIALMGETVGVSKESKHIWK 734
Db      646  KFTIGMDLFTENYRFKSVFVILLVYVILLTYIILLNMLIALMGETVSKIAQESKSIWK 705
QY      735  LQ 736
Db      706  LQ 707

```

Search completed: December 2, 2004, 22:26:45
 Job time : 206 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:36:21 ; Search time 43 Seconds

(without alignments)
1660.299 Million cell updates/sec

Title: US-10-090-215-12

Sequence: 742

Sequence: 1 MADSSRGPRAGFGEVAFLEPG.....GVSKSKSHIMKLQSGRRLL 742

Scoring table:

Gapco 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	2.2	838	2	T09054
2	16	2.2	839	2	JC7621
3	8	1.1	79	2	H58933
4	8	1.1	143	2	F95116
5	8	1.1	143	2	D97985
6	8	1.1	213	2	A56152
7	8	1.1	213	2	AC3408
8	8	1.1	252	1	H69002
9	8	1.1	286	2	C64538
10	8	1.1	334	2	A12150
11	8	1.1	341	2	A52445
12	8	1.1	379	2	A55130
13	8	1.1	379	2	G98000
14	8	1.1	484	2	F71317
15	8	1.1	496	2	T44987
16	8	1.1	550	2	C86348
17	8	1.1	618	2	A75469
18	8	1.1	688	2	H83070
19	8	1.1	723	2	UC7795
20	8	1.1	725	2	UC7531
21	8	1.1	727	2	JC7796
22	8	1.1	1454	2	T13709
23	7	0.9	31	2	S00685
24	7	0.9	55	2	E81500
25	7	0.9	80	2	B69157
26	7	0.9	90	2	H87544
27	7	0.9	96	2	T28327
28	7	0.9	111	2	H72707
29	7	0.9	117	2	I38362

ALIGNMENTS

30	7	0.9	122	2	H70176	hypothetical prote
31	7	0.9	138	2	S59128	trp-like protein -
32	7	0.9	145	1	J00947	atrial natriuretic
33	7	0.9	147	2	A37763	viadl protein - Ag
34	7	0.9	147	2	AC3250	viadl/G regulated p
35	7	0.9	149	2	S50683	viadl protein - Ag
36	7	0.9	149	2	S59129	trp-1ike protein -
37	7	0.9	160	2	D75388	NADH2 dehydrogenas
38	7	0.9	170	2	T08348	hypothetical prote
39	7	0.9	178	2	S76780	hypothetical prote
40	7	0.9	179	2	AE2225	hypothetical prote
41	7	0.9	195	2	B97050	guanylate kinase (
42	7	0.9	207	2	AF0199	probable lipoprote
43	7	0.9	210	2	AF1192	two component resp
44	7	0.9	222	2	F82420	arginine ABC trans
45	7	0.9	224	2	F84239	hypothetical prote

RESULT 1

T09054 capsacin receptor - rat

N/Alternate names: vanilloid receptor subtype 1

C/Species: Rattus norvegicus (Norway rat)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T09054

R/Caterina, M.J.; Schumacher, M.A.; Tomimaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D

Nature 389, 816-824, 1997

A/Title: The capsacin receptor: A heat-activated ion channel in the pain pathway.

A/Reference number: Z16539; MUID:98007969; PMID:9349813

A/Accession: T09054

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-838 <CAT>

A/Cross-references: UNIPROT:Q35433; EMBL:AF029310; NID:92570932; PIDN:AC53398.1; PID:G

A/Experimental source: dorsal root ganglion

C/Keywords: ion channel; receptor

Query Match	2.2%	Score 16;	DB 2;	Length 838;
Best Local Similarity	100.0%;	Pred. No. 1.1e-07;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	282	FFFGELPLSLAAGTNO	297	
Db	245	FFFGELPLSLAAGTNO	260	

RESULT 2

JC7621

capsacin receptor, VR1 - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C/Accession: JC7621

R/Cortright, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.

Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001

A/Title: The tissue distribution and functional characterization of human VR1.

A/Reference number: JC7621; MUID:21139751; PMID:11243859

A/Contents: Dorsal root ganglia

A/Accession: JC7621

A/Molecule type: mRNA

A/Residues: 1-839 <COR>

A/Cross-references: UNIPROT:Q9H304; GB:AF196175

C/Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a

its integrative activation by several noxious stimuli, and plays an important role in

C/Keywords: transmembrane protein

A/Map position: 17p13

C/Keywords: ankyrin #status predicted <ANK1>

F:248-280/Domain: ankyrin #status predicted <ANK2>

F:333-365/Domain: ankyrin #status predicted <ANK3>

F:433-455/Domain: transmembrane #status predicted <TM1>
 F:477-495/Domain: transmembrane #status predicted <TM2>
 F:508-531/Domain: transmembrane #status predicted <TM3>
 F:543-569/Domain: transmembrane #status predicted <TM4>
 F:578-597/Domain: transmembrane #status predicted <TM5>
 F:624-644/Region: pore loop #status predicted
 F:656-684/Domain: transmembrane #status predicted <TM6>

Query Match 2.2%; Score 16; DB 2; Length 839;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLACTNQ 297
 DB 246 FYFGEPLSLACTNQ 261

RESULT 3

H58933
 succinate dehydrogenase hydrophobic subunit - Cyanidioschyzon merolae mitochondrion
 C:Species: mitochondrion Cyanidioschyzon merolae
 C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C:Accession: H58933

R:Ohta, N.; Sato, N.; Kuroiwa, T.
 Nucleic Acids Res. 26, 5190-5198, 1998
 A:Title: Structure and organization of the mitochondrial genome of the unicellular red alga *Cyanidioschyzon merolae*
 A:Reference number: A58930; MUID:99030526; PMID:9801318

A:Accession: H58933
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-79 <ARN>

A:Cross-references: UNIPROT:Q9ZZN2; GB:D89861; NID:94115781; PIDN:BAA36542.1; PID:dl0375
 C:Genetics:
 A:Gene: sdhd
 A:genome: mitochondrion
 C:Keywords: mitochondrion

Query Match 1.1%; Score 8; DB 2; Length 79;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 FLIVVILF 624
 DB 72 FLIVVILF 79

RESULT 4

F95116
 GtrA family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: F95116
 R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple, neon, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a Virulent Isolate of *Streptococcus pneumoniae*.
 A:Reference number: A95000; MUID:21357209; PMID:11463926

A:Accession: F95116
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-143 <KUR>

A:Cross-references: UNIPROT:Q97R28; GB:AE005672; PIDN:AAK75127.1; PID:gl4972484; GSPDB:C
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP1011

Query Match 1.1%; Score 8; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 STFLDLF 674

DB 85 STFLDLF 92

RESULT 5

D97986
 mesh protease [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: D97986

R:Hoekstra, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Ee, R.; LeBlanc, D.J.; Lee, L.N.; Letkovitz, E.J.; Lu, J.; Matsushima, P.; Mohren, S.; M
 Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: D97986
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-143 <KUR>

A:Cross-references: UNIPROT:Q8DQ02; GB:AE007317; PIDN:AAK9720.1; PID:gl5458524; GSPDB:C
 C:Genetics:
 A:Gene: mesh

Query Match 1.1%; Score 8; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 STFLDLF 674
 DB 85 STFLDLF 92

RESULT 6

A56152
 major 25k outer membrane protein precursor - Brucella abortus
 C:Species: Brucella abortus
 C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C:Accession: A56152

R:de Wergifosse, P.; Lintermans, P.; Limer, J.N.; Cloeckaert, A.
 J. Bacteriol. 177, 1911-1914, 1995
 A:Title: Cloning and nucleotide sequence of the gene coding for the major 25-kilodalton
 A:Reference number: A56152; MUID:95204367; PMID:7896724

A:Accession: A56152
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-213 <DEA>

A:Cross-references: UNIPROT:Q44664; GB:X79284; NID:9769744; PIDN:CAAS5872.1; PID:g769745
 Query Match 1.1%; Score 8; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 LVIVSAL 566
 DB 7 LVIVSAL 14

RESULT 7

AC3408
 25k outer-membrane immunogenic protein precursor [imported] - Brucella melitensis (strain
 C:Species: Brucella melitensis
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AC3408

R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ios, T.; Ivanova,
 ; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letic
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen *Brucella meliten*
 A:Reference number: AD3252; PMID:11756688

A:Accession: AC3408
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-213 <KUR>
 A:Cross-references: UNIPROT:Q45321; GB:AE008917; PIDN:AAL52430.1; PID:G17983234; GSPDB:G
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME11249
 A:Map position: 1

Query Match 1.1%; Score 8; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 559 LVIYSAAL 566
 DB 7 LVIYSAAL 14

RESULT 8
 H69002
 conserved hypothetical protein MTH1019 - Methanobacterium thermoautotrophicum (strain De
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Dec-2002
 C:Accession: H69002
 R:Smith, D.R.; Doucette-Stramm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 K., S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: H69002
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-252 <MTH>
 A:Cross-references: GB:AE000874; GB:AE000666; NID:G2622110; PIDN:AAB85515.1; PID:G262212
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1019
 C:Superfamily: uncharacterized conserved protein

Query Match 1.1%; Score 8; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 214 LDIAERTG 221
 DB 68 LDIAERTG 75

RESULT 9
 C64538
 cytochrome-c oxidase (EC 1.9.3.1) chain fixp - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: C64538
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKenna
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Delman, J.M.; Fujii, C.; Bowman, C.; Watney, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: C64538
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-286 <TOM>
 A:Cross-references: UNIPROT:Q24958; GB:AE000536; GB:AE000511; NID:G2313230; PIDN:AAD0721
 C:Superfamily: cytochrome c oxidase, cbh3-type, fixp subunit, cytochrome c6 homology
 C:Keywords: chromoprotein; electron transfer; heme; iron; membrane-associated complex; m
 F:128/132/Binding site: heme (Cys) (covalent) #status predicted
 F:133/Binding site: heme iron (His) (axial ligand) #status predicted
 F:219/222/Binding site: heme (Cys) (covalent) #status predicted
 F:223/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 1.1%; Score 8; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KALNLSN 204
 DB 278 KALNLSN 285

RESULT 10
 A12150
 serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: A12150
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguch
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: A12150
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-334 <KUR>
 A:Cross-references: UNIPROT:Q8YTF7; GB:BA000019; PIDN:BAW74459.1; PID:G17131853; GSPDB
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: al12760

Query Match 1.1%; Score 8; DB 2; Length 334;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 432 SVLETLVY 439
 DB 129 SVLETLVY 136

RESULT 11
 AE2445
 hypothetical protein alr5117 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AE2445
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguch
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2445
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-341 <KUR>
 A:Cross-references: UNIPROT:Q8YVW24; GB:BA000019; PIDN:BAW76816.1; PID:G17134255; GSPDB:
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr5117
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 1.1%; Score 8; DB 2; Length 341;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 286 ELPISTAA 293
 DB 136 ELPISTAA 143

RESULT 12
 A95130
 glycogen biosynthesis protein G1gd [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C/Accession: A95130
 R/Retireltn, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held
 mon, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 Science 293, 498-506, 2001
 A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A/Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
 A/Reference number: A95000; MIMD:21557209; PMID:11463916
 A/Accession: A95130
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-379 <KUR>
 A/Cross-references: UNIPROT:Q970S6; GB:AE005672; PIDN:AAK75234.1; PID:G14972600; GSPDB:Q
 C/Genetics: 8
 A/Experimental source: strain TIGR4
 A/Genes: SP123

Query Match 1.1%; Score 8; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 FPLSSIAN 38
 Db 42 FPLSSIAN 49

RESULT 13
 G98000
 required for glycogen biosynthesis [imported] - *Streptococcus pneumoniae* (strain R6)
 C/Species: *Streptococcus pneumoniae*
 C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C/Accession: G98000
 R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; DeHoff, B.S.; E
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A/Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
 A/Reference number: A97872; MIMD:21429245; PMID:11544234
 A/Accession: G98000
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-379 <KUR>
 A/Cross-references: UNIPROT:Q9BPS4; GB:AE007317; PIDN:AAK99835.1; PID:G15458649; GSPDB:Q
 C/Genetics: 8
 A/Experimental source: strain TIGR4
 A/Genes: 919D

Query Match 1.1%; Score 8; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 FPLSSIAN 38
 Db 42 FPLSSIAN 49

RESULT 14
 F71317
 probable antigen, p83/100 - syphilis spirochete
 C/Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C/Accession: F71317
 R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 reon, J.; Khakak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McD
 they, L.; Weidman, U.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A/Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A/Reference number: A71250; MIMD:98332770; PMID:9665876
 A/Accession: F71317
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-484 <COL>

A/Cross-references: UNIPROT:O81499; GB:AE001225; GB:AE000520; NID:G3322775; PIDN:AAK6547
 A/Experimental source: strain Nichols
 C/Genetics: 8
 A/Genes: TP0486

Query Match 1.1%; Score 8; DB 2; Length 484;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 HALVALIND 333
 Db 418 HALVALIND 425

RESULT 15
 T44987
 aldehyde dehydrogenase (EC 1.2.1.-) [imported] - *Haloflex volcanii* megaplasmid pHV3
 C/Species: *Haloflex volcanii*
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T44987
 R/Farham, R.; Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Charlebois, R.L.
 submitted to the EMBL Data Library, March 1997
 A/Description: Hereditary instability of the megaplasmid pHV3, and filamentation in the
 A/Reference number: Z22886
 A/Accession: T44987
 A/Status: preliminary; translated from GB/EMBL/DDBI
 A/Molecule type: DNA
 A/Residues: 1-496 <FAR>
 A/Cross-references: UNIPROT:O34184; EMBL:U95374; PIDN:AAK71806.1
 A/Experimental source: strain DS2
 C/Genetics: 8
 A/Map position: megaplasmid pHV3
 A/Note: expressed during exponential growth
 A/Suprafamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
 C/Keywords: oxidoreductase

Query Match 1.1%; Score 8; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 GSTRADLDG 168
 Db 360 GSTRADLDG 367

Search completed: December 2, 2004, 22:46:26
 Job time: 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:27:41 ; Search time 203 Seconds

(without alignments)
2103.094 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 742
Sequence: 1 MADSSGPRAGPGEVAELPG.....GQVSKSKXHWLQSGRRRL 742

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	99.2	853	2	Q86YZ6
2	736	99.2	871	2	Q8NDY7
3	736	99.2	871	2	Q9HBC0
4	736	99.2	871	2	Q96C92
5	668	90.0	803	2	Q96RS7
6	635	85.6	871	2	Q9HBA0
7	384	51.8	811	2	Q8NG64
8	181	24.4	871	2	Q9ERZ8
9	112	15.1	803	2	Q91XR5
10	112	15.1	871	2	Q9EPK8
11	112	15.1	871	2	Q9ROZ4
12	112	15.1	871	2	Q9RS76
13	112	15.1	873	2	Q9ERZ7
14	68	9.2	852	2	Q9DF53
15	28	3.8	528	2	Q9Z182
16	19	2.6	103	2	Q8RET8
17	19	2.6	195	2	Q9SLU9
18	19	2.6	195	2	Q8NET9
19	19	2.6	790	2	Q8NDW7
20	19	2.6	790	2	Q8NFW2
21	19	2.6	791	2	Q8NET8
22	19	2.6	791	2	Q8K424
23	16	2.2	468	2	Q9Z0B4
24	16	2.2	511	2	Q9H303
25	16	2.2	778	2	Q9UM56
26	16	2.2	838	2	Q35433
27	16	2.2	839	2	Q9JMS7
28	16	2.2	839	2	Q8NER1
29	16	2.2	839	2	Q9NC74
30	16	2.2	839	2	Q9NY22
31	16	2.2	839	2	Q9H0G9

32	16	2.2	839	2	Q9H304	Q9H304 homo sapien
33	16	2.2	839	2	Q6R5A3	Q6R5A3 cavia porce
34	16	2.2	839	2	Q704Y3	Q704Y3 mus musculu
35	16	2.2	839	2	Q8K1W1	Q8K1W1 cavia porce
36	16	2.2	839	2	AAS13460	AAS13460 cavia por
37	16	2.2	839	2	CAF05661	CAF05661 mus muscu
38	16	2.2	839	2	BAD20301	BAD20301 mus muscu
39	16	2.2	842	2	Q6RX08	Q6RX08 oryctolagus
40	16	2.2	842	2	AAR34458	AAR34458 oryctolag
41	16	2.2	843	2	Q8QFN9	Q8QFN9 gallus gall
42	14	1.9	151	2	Q81Z19	Q81Z19 homo sapien
43	14	1.9	471	2	Q9JLM0	Q9JLM0 rattus norv
44	14	1.9	756	2	Q60GX2	Q60GX2 f-11 rat/mo
45	14	1.9	756	2	Q9WTR1	Q9WTR1 mus musculu

ALIGNMENTS

RESULT 1	ID	Q86YZ6	PRELIMINARY	PRT	653 AA.
AC	Q86YZ6	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Hypothetical protein TRPV-SV.				
GN	Name=TRPV-SV.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Suzuki S.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Suzuki M.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, AB100308; BAC55864.1; --				
DR	GO; GO:0016021; C:Integral to membrane; IEA.				
DR	GO; GO:0005261; F:Cation channel activity; IEA.				
DR	GO; GO:0006812; P:Cation transport; IEA.				
DR	InterPro: IPR002110; ANK.				
DR	InterPro: IPR002111; Cat. channel TrpL.				
DR	InterPro: IPR008996; CytoK_IL1_like.				
DR	InterPro: IPR005821; Ion trans.				
DR	InterPro: IPR004729; TRPChannel.				
DR	InterPro: IPR008347; Vanil receptor.				
DR	InterPro: IPR008348; Vanil_receptor2.				
DR	Pfam: PF00023; Ank. 3.				
DR	Pfam: PF00520; Ion_trans. 1.				
DR	PRINTS: PR01415; ANKRIN.				
DR	PRINTS: PR01768; TRPVRECEPTOR.				
DR	PRINTS: PR01769; VRL2RECEPTOR.				
DR	SMART: SM00248; ANK. 3.				
DR	TIGRFAMs: TIGR00870; trp. 1.				
DR	PROSITE: PS50088; ANK_REPEAT. 1.				
DR	PROSITE: PS50297; ANK_REPEAT_REGION. 1.				
KW	ANK repeat; Hypothetical protein; Ion transport; Ionic channel; Transmembrane; Transport.				
SQ	SEQUENCE 853 AA; 96448 MW; EAA07196606AED20 CRC64;				
QY	Query Match	99.2%;	Score 736;	DB 2;	Length 853;
QY	Best Local Similarity	100.0%;	Pred. No. 0;		
QY	Matches	736;	Conservative	0;	Mismatches
QY	1	MADSSGPRAGPGEVAELPGDESGTPGGEAPFLSIANIPEGSDGSLSPSPADARPGAP	60		
DB	1	MADSSGPRAGPGEVAELPGDESGTPGGEAPFLSIANLFGSDGSLSPSPADARPGAP	60		
QY	61	GDGRENLMKFGAERKGVNPFIDLLSTYESSVVPGPCKAPMDSLFDYGTGRHSSDN	120		

Db	61	GDGRPELRKMKFGQAFKGVNPIDLLSTLISSVSPQKAPMDSLPDYGTIRHSSDN	120
Qy	121	KRRRRKTIKKOPQSPKAPAPQPPPIIKVFNRRILEDIVSRGSTADLDGLPFLITRRKRL	180
Db	121	KRRRRKTIKKOPQSPKAPAPQPPPIIKVFNRRILEDIVSRGSTADLDGLPFLITRRKRL	180
Qy	181	TDEEFPSPSTGKTCLEPKALLNSNGNDPTPLDIARTGNMSEFNSPRDIYVNGOT	240
Db	181	TDEEFPSPSTGKTCLEPKALLNSNGNDPTPLDIARTGNMSEFNSPRDIYVNGOT	240
Qy	241	ALHAIATERCKHYVELLVLAQADVHAQARGFPQKDGAFYFGELPLSLAATCNPPIH	300
Db	241	ALHAIATERCKHYVELLVLAQADVHAQARGFPQKDGAFYFGELPLSLAATCNPPIH	300
Qy	301	VNLTLENPKKKADMRQDSRGNTVLAHALVALDNTRENTKVTYKMDLLIKCARLEPDS	360
Db	301	VNLTLENPKKKADMRQDSRGNTVLAHALVALDNTRENTKVTYKMDLLIKCARLEPDS	360
Qy	361	NLEAVLNNDGLSPILMMAAKTGKIGIFQHIIRREVTDEDTRELSRFKDMAAGPYSSLYD	420
Db	361	NLEAVLNNDGLSPILMMAAKTGKIGIFQHIIRREVTDEDTRELSRFKDMAAGPYSSLYD	420
Qy	421	LSLSDTGCGEASVLEILVYNSKIKENRHEMLAVEPINELLRDKMRKFGASVYINVSYL	480
Db	421	LSLSDTGCGEASVLEILVYNSKIKENRHEMLAVEPINELLRDKMRKFGASVYINVSYL	480
Qy	481	AMVIFLTLLAVYQGLDETPPYPRRTYDYLRLAGEYITLFTGVLPEFTNIKQLPKKKPGV	540
Db	481	AMVIFLTLLAVYQGLDETPPYPRRTYDYLRLAGEYITLFTGVLPEFTNIKQLPKKKPGV	540
Qy	541	NSLFDIGSPQLLFFYISVLYVISAALYLAGIEAVLAVWFAVLVGMMNALYFTGKLKLTG	600
Db	541	NSLFDIGSPQLLFFYISVLYVISAALYLAGIEAVLAVWFAVLVGMMNALYFTGKLKLTG	600
Qy	601	TSYIMTOKILFKQLRFFLLVYLLFMIGVSAVSLINPCAMKKNENQNTCTPTPSC	660
Db	601	TSYIMTOKILFKQLRFFLLVYLLFMIGVSAVSLINPCAMKKNENQNTCTPTPSC	660
Qy	661	RDESESTFLLDLFEKLTIGMGDELMSSKPYVVEFIILLVYIILTEVLLNMLIALMGE	720
Db	661	RDESESTFLLDLFEKLTIGMGDELMSSKPYVVEFIILLVYIILTEVLLNMLIALMGE	720
Qy	721	TVGQVSKESKHIMKLG 736	
Db	721	TVGQVSKESKHIMKLG 736	
RESULT 2			
QBNBY7		PRELIMINARY; PRT; 871 AA.	
AC	QBNBY7		
DT	01-OCT-2002 (TREMBLrel. 22, Created)		
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Vanilloid receptor-like channel 2.		
GN	Name=VRL2;		
OS	Homio sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22107054; Pubmed=12077606;		
RA	Smith G.D., Gunthorpe M.D., Kelsell R.E., Hayes P.D., Reilly P.,		
RA	Facer P.J., Wright J.E., Jerman J.C., Walhin J-P., Ooi U., Egerton J.,		
RA	Charlier K.J., Smart D., Randall A.D., Anand P., Davis J.B.;		
RT	"TRPV3 is a temperature-sensitive vanilloid receptor-like protein.";		
RL	Nature 418:186-190(2002).		
DR	EMBL, AJ296305; CAC82937.1; --		
DR	Genew; HGNC:18083; TRPV4.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005261; F:cation channel activity; IEA.		

Query	Match	99.2%	Score 736;	DB 2;	Length 871;	
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Db	1	MADSSSEGPRAAGPGVAELPGDESGTGGGEAPPLSLANI	FGEDGSLSPSPADASRPAGP	60		GO: GO:0004872; F:receptor activity; IEA.
Qy	1	MADSSSEGPRAAGPGVAELPGDESGTGGGEAPPLSLANI	FGEDGSLSPSPADASRPAGP	60		GO: GO:0006812; P:cation transport; IEA.
Db	61	GDGPPNLRMKQGAFRKGVNPIDLBESTLYESSVPEPKAPMDSL	LDYGYRHHSSDN	120		DR GO: InterPro: IPR002110; ANK.
Qy	61	GDGPPNLRMKQGAFRKGVNPIDLBESTLYESSVPEPKAPMDSL	LDYGYRHHSSDN	120		DR InterPro: IPR002111; Cat. channel_TypL.
Db	61	GDGPPNLRMKQGAFRKGVNPIDLBESTLYESSVPEPKAPMDSL	LDYGYRHHSSDN	120		DR InterPro: IPR008996; Cytok_IL1_like.
Qy	121	KRWKRTIIEKQOPAKAPAPPPILTKYENRPI	FDIYSRGSADLDGLPELTHKKRL	180		DR InterPro: IPR005821; Ion channel.
Db	121	KRWKRTIIEKQOPAKAPAPPPILTKYENRPI	FDIYSRGSADLDGLPELTHKKRL	180		DR InterPro: IPR004729; TRPchannel.
Qy	121	KRWKRTIIEKQOPAKAPAPPPILTKYENRPI	FDIYSRGSADLDGLPELTHKKRL	180		DR InterPro: IPR008347; Vanil_receptor.
Db	121	KRWKRTIIEKQOPAKAPAPPPILTKYENRPI	FDIYSRGSADLDGLPELTHKKRL	180		DR InterPro: IPR008348; Vanil_receptor2.
Qy	181	TDEEFPREBSTGTCPLPKALLMSGRNDTIPVLLDIAERTGNMRE	FINSPRPDIYYRGQT	240		DR Pfam: PF00023; ANK; 3.
Db	181	TDEEFPREBSTGTCPLPKALLMSGRNDTIPVLLDIAERTGNMRE	FINSPRPDIYYRGQT	240		DR Pfam: PF00520; Ion_trans; 1.
Qy	181	TDEEFPREBSTGTCPLPKALLMSGRNDTIPVLLDIAERTGNMRE	FINSPRPDIYYRGQT	240		DR PRINTS: PRO1415; ANKRYN.
Db	181	TDEEFPREBSTGTCPLPKALLMSGRNDTIPVLLDIAERTGNMRE	FINSPRPDIYYRGQT	240		DR PRINTS: PRO1768; TREPRECEPTOR.
Qy	241	ALHAIARERCHAYEILVAQADVHAQGRFPQPKDGGYFYGELPLSLA	CNOGHI	300		DR PRINTS: PRO1769; VRL2RECEPTOR.
Db	241	ALHAIARERCHAYEILVAQADVHAQGRFPQPKDGGYFYGELPLSLA	CNOGHI	300		DR SMART: SM00248; ANK; 3.
Qy	301	VNYLTLENHKKADMRQDSRGNTVLAHALADNTRENTKFTVXYDILL	KCARLPDS	360		DR TIGRFAMs: TIGR00870; trp; 1.
Db	301	VNYLTLENHKKADMRQDSRGNTVLAHALADNTRENTKFTVXYDILL	KCARLPDS	360		DR PROSITE: PS50088; ANK_REPEAT; 1.
Qy	301	VNYLTLENHKKADMRQDSRGNTVLAHALADNTRENTKFTVXYDILL	KCARLPDS	360		DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
Db	301	VNYLTLENHKKADMRQDSRGNTVLAHALADNTRENTKFTVXYDILL	KCARLPDS	360		DR ANK_repeat; Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
Qy	361	NLEAVLNNDGSLPLMAAKTKIGIFGHIIRREVVDENGRHLSRKFQWAGPYVSS	LYD	420		SEQUENCE 871 AA; 98280 MW; C62056B86C5A6FB6 CRC64;
Db	361	NLEAVLNNDGSLPLMAAKTKIGIFGHIIRREVVDENGRHLSRKFQWAGPYVSS	LYD	420		
Qy	421	LSLSDTCGEASVLEILVYNSKIENRHEMLAVEPINEILLRDKMRKFGAVSFYIN	YSYC	480		
Db	421	LSLSDTCGEASVLEILVYNSKIENRHEMLAVEPINEILLRDKMRKFGAVSFYIN	YSYC	480		
Qy	481	AMVIFTLTAYYOPILEGTPPYRTVDYLRAGEVITLFTGLFFFTNIKDLFMKKCP	DEV	540		
Db	481	AMVIFTLTAYYOPILEGTPPYRTVDYLRAGEVITLFTGLFFFTNIKDLFMKKCP	DEV	540		
Qy	541	NSLFDIGSFOLLYFYISVIVISALYAGIEAYAVWVAFVLGOMNALY	YTRGKLTG	600		
Db	541	NSLFDIGSFOLLYFYISVIVISALYAGIEAYAVWVAFVLGOMNALY	YTRGKLTG	600		
Qy	601	TYSIMIQKILFKDILFRLLVYLLFMIGASALVSLINPCANMKVCNE	DTCTVTPYPSG	660		
Db	601	TYSIMIQKILFKDILFRLLVYLLFMIGASALVSLINPCANMKVCNE	DTCTVTPYPSG	660		
Qy	661	RDSEFFSFRLDLFLKTLGMDGLEMLSTKKPVVYIILLVYIILTFVLL	INMLALAME	720		
Db	661	RDSEFFSFRLDLFLKTLGMDGLEMLSTKKPVVYIILLVYIILTFVLL	INMLALAME	720		

QY 721 TVGVSKSKSHIWKIQ 736
 DB 721 TVGVSKSKSHIWKIQ 736

RESULT 3

Q9HBCO PRELIMINARY; PRT; 871 AA.
 AC Q9HBCO; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE OTRPC4
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Renal cortex;
 RX MEDLINE=20482174; PubMed=11025659;
 RA Strickman R., Harteneck C., Nunnemacher K., Schultz G., Plant T.D.:
 "OTRPC4, a nonselective cation channel that confers sensitivity to
 extracellular osmolarity."
 RT Nat. Cell Biol. 2:695-702(2000).
 RL EMBL, AF258465; AAG16127.1; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0015281; F:nonselective cation channel activity; NAS.
 DR GO; GO:0006816; P:calcium ion transport; NAS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR008996; CytoK_IL1_like.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion_trans; 1.
 DR PRINTS; PRO1415; ANKYRIN.
 DR PRINTS; PRO1768; TRPVRECEPTOR.
 DR PRINTS; PRO1769; VRL2RECEPTOR.
 DR SMART; SMO0248; ANK; 3.
 DR TIGRFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR KAM repeat; Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 871 AA; 98294 MW; C62056B86DEA6F86 CRC64;

Query Match 99.2%; Score 736; DB 2; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSSEGRAGPGEVAELPGDESGTPGGEAFPLSLIANTFEGEGGSLSPSPADSRPAGP 60
 DB 1 MADSSSEGRAGPGEVAELPGDESGTPGGEAFPLSLIANTFEGEGGSLSPSPADSRPAGP 60
 QY 61 GDGRPNLRMKFQGAERKGVNPDIDLLESTLYESSVVGPKKAPMDSLFDYTYRHSSDN 120
 DB 61 GDGRPNLRMKFQGAERKGVNPDIDLLESTLYESSVVGPKKAPMDSLFDYTYRHSSDN 120
 QY 121 KRWKKKTIIEKOPQSPKAPAPPPPIILVFNNPILFDIVSRGSTADLDGLPFLLTHKKRL 180
 DB 121 KRWKKKTIIEKOPQSPKAPAPPPPIILVFNNPILFDIVSRGSTADLDGLPFLLTHKKRL 180
 QY 181 TDEEFREPSTGKTCLPALNLISGRNDTTPVLIDIAERTGMNMFINSPPROTYVGGOT 240
 DB 181 TDEEFREPSTGKTCLPALNLISGRNDTTPVLIDIAERTGMNMFINSPPROTYVGGOT 240
 QY 241 ALHAIIRRCCKHYVELLVAOCADVHAQARGFPQKDEGGYFYFGLPLSLAATNPHI 300
 DB 241 ALHAIIRRCCKHYVELLVAOCADVHAQARGFPQKDEGGYFYFGLPLSLAATNPHI 300

QY 301 VNYLTENPKKADMRRODSRGNTVLAVALADNTRNTKFTYKMYDLILKCARLPDS 360
 DB 301 VNYLTENPKKADMRRODSRGNTVLAVALADNTRNTKFTYKMYDLILKCARLPDS 360
 QY 361 NLEAVLNDGSLPIMAAATGKIGIFQHIIRBVDDETRHSRKFKDWAYGVYSLYD 420
 DB 361 NLEAVLNDGSLPIMAAATGKIGIFQHIIRBVDDETRHSRKFKDWAYGVYSLYD 420
 QY 421 LSLDTCGEASVLELVVNSKIENRHEMLAEPINELLROKWRKGAVSFYINVSYL 480
 DB 421 LSLDTCGEASVLELVVNSKIENRHEMLAEPINELLROKWRKGAVSFYINVSYL 480
 QY 481 AMVIFTLTAAYOPLBGTPEPPYRTTYDYLRLAGEVITLFTGVLPFTNKKDIPMKKCPGV 540
 DB 481 AMVIFTLTAAYOPLBGTPEPPYRTTYDYLRLAGEVITLFTGVLPFTNKKDIPMKKCPGV 540
 QY 541 NSLFTDGSFQILYFYISLVIVSALVLAGIBAYLAWVFALVGMNVALFTRGKLKG 600
 DB 541 NSLFTDGSFQILYFYISLVIVSALVLAGIBAYLAWVFALVGMNVALFTRGKLKG 600
 QY 601 TYSIMIOKILFEDLFRFLVYLLFMIGYASALVSLNRCANMKVCNEDQCTVPYPSG 660
 DB 601 TYSIMIOKILFEDLFRFLVYLLFMIGYASALVSLNRCANMKVCNEDQCTVPYPSG 660
 QY 661 RDSERTSTFLDLFLITIGMDLEMLSTKYPVVFIILVTYIILFTVLLNMLALMGE 720
 DB 661 RDSERTSTFLDLFLITIGMDLEMLSTKYPVVFIILVTYIILFTVLLNMLALMGE 720
 QY 721 TVGVSKSKSHIWKIQ 736
 DB 721 TVGVSKSKSHIWKIQ 736

RESULT 4

Q96G92 PRELIMINARY; PRT; 871 AA.
 AC Q96G92;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Vanilloid receptor like channel-2.
 GN Name=VRL-2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC Ieshibashi K.;

RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB032427; BAB69040.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR008996; CytoK_IL1_like.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion_trans; 1.
 DR PRINTS; PRO1415; ANKYRIN.
 DR PRINTS; PRO1768; TRPVRECEPTOR.
 DR PRINTS; PRO1769; VRL2RECEPTOR.
 DR SMART; SMO0248; ANK; 3.
 DR TIGRFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR KAM repeat; Ion transport; Ionic channel; Receptor; Transmembrane; Transport.

SQ SEQUENCE 871 AA; 98266 MW; C62056A401ECA8B6 CRC64;
 Query Match 99.2%; Score 736; DB 2; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGRAGGAEVALPGDESGTGGGEAFPLSLANLFEDEGDSLSPSPADSRPAGP 60
 DB 1 MADSEGRAGGAEVALPGDESGTGGGEAFPLSLANLFEDEGDSLSPSPADSRPAGP 60
 QY 61 GDGRNLMKFKGAEVAPKGVNPIIDLESTLYESSVVPQPKAPMDSLFDYGYRHHSSDN 120
 DB 61 GDGRNLMKFKGAEVAPKGVNPIIDLESTLYESSVVPQPKAPMDSLFDYGYRHHSSDN 120
 QY 121 KMRKKIIEKQPSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
 DB 121 KMRKKIIEKQPSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
 QY 121 KMRKKIIEKQPSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
 DB 121 KMRKKIIEKQPSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
 QY 181 TDEFRBESTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPRDIYRGQT 240
 DB 181 TDEFRBESTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPRDIYRGQT 240
 QY 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDSGTYFGELPLSLAAGTNOPIH 300
 DB 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDSGTYFGELPLSLAAGTNOPIH 300
 QY 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDSGTYFGELPLSLAAGTNOPIH 300
 DB 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDSGTYFGELPLSLAAGTNOPIH 300
 QY 301 VNYLTENPKKADMRRODSRGNTVLAIVAIADNTRNTKFTVKNYDILLKCARLFPDS 360
 DB 301 VNYLTENPKKADMRRODSRGNTVLAIVAIADNTRNTKFTVKNYDILLKCARLFPDS 360
 QY 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTEDETRHLSRKKQWAGPYVSSLYD 420
 DB 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTEDETRHLSRKKQWAGPYVSSLYD 420
 QY 421 LSLDTCGEASVLELTVNSKIENHEMLAVEPINELLRDKMRKGAVSFYINVSYSYC 480
 DB 421 LSLDTCGEASVLELTVNSKIENHEMLAVEPINELLRDKMRKGAVSFYINVSYSYC 480
 QY 481 ANVIFLTAYQPLESTPPYRTTVDYRIAGEVITLFTGVLFPTNLIKDLFMKKCPGV 540
 DB 481 ANVIFLTAYQPLESTPPYRTTVDYRIAGEVITLFTGVLFPTNLIKDLFMKKCPGV 540
 QY 541 NSLFDIGSFQLYFISVAVISALYLAGIEAVLAVMVFALVGMNNAVYFTRGLKLTG 600
 DB 541 NSLFDIGSFQLYFISVAVISALYLAGIEAVLAVMVFALVGMNNAVYFTRGLKLTG 600
 QY 601 TYSIMTQKILFKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 DB 601 TYSIMTQKILFKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
 QY 661 RDESESTFLLDKLTIGMDLEMLSTKYPVVFIIILVTYIILFVLLNMLALMGE 720
 DB 661 RDESESTFLLDKLTIGMDLEMLSTKYPVVFIIILVTYIILFVLLNMLALMGE 720
 QY 721 TVGQVSKESKHIWKLQ 736
 DB 721 TVGQVSKESKHIWKLQ 736

RESULT 5
 Q96RS7 PRELIMINARY; PRT; 803 AA.
 AC Q96RS7;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Vanilloid receptor-like protein 2.
 GN Name=VRL2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Deret C., Schaffer M.K.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF279673; AAK69487.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; F:receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR Interpro; IPR002110; ANK.
 DR Interpro; IPR002111; Cat channel TrpL.
 DR Interpro; IPR008996; CytoK IL1 like.
 DR Interpro; IPR004729; Ion trans.
 DR Interpro; IPR008347; Vanil_receptor.
 DR Interpro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PRO1415; ANKYRIN.
 DR PRINTS; PRO1768; TRPVRECEPTOR.
 DR PRINTS; PRO1769; VRL2RECEPTOR.
 DR SMART; SM00248; ANK; 3.
 DR TIGRFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KW transport.
 SQ SEQUENCE 803 AA; 91635 MW; AB329C595B325784 CRC64;

Query Match 90.0%; Score 668; DB 2; Length 803;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 MKFGAERKGVNPIIDLESTLYESSVVPQPKAPMDSLFDYGYRHHSSDNKMRKKI 128
 DB 1 MKFGAERKGVNPIIDLESTLYESSVVPQPKAPMDSLFDYGYRHHSSDNKMRKKI 60
 QY 129 EKQPSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRLTDEFRBP 188
 DB 61 EKQPSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRLTDEFRBP 120
 QY 189 STGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPRDIYRGQALHAIER 248
 DB 121 STGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFINSPPRDIYRGQALHAIER 180
 QY 249 RCKHYVELVAQADVAHQARGFPOPKDSGTYFGELPLSLAAGTNOPIHNTENP 308
 DB 181 RCKHYVELVAQADVAHQARGFPOPKDSGTYFGELPLSLAAGTNOPIHNTENP 240
 QY 309 HKKADMRRODSRGNTVLAIVAIADNTRNTKFTVKNYDILLKCARLFPDSNLEAVLN 368
 DB 241 HKKADMRRODSRGNTVLAIVAIADNTRNTKFTVKNYDILLKCARLFPDSNLEAVLN 300
 QY 369 DGLSPMLMAAKTGKIGIFQHIIRREVTEDETRHLSRKKQWAGPYVSSLYDLSLDTG 428
 DB 301 DGLSPMLMAAKTGKIGIFQHIIRREVTEDETRHLSRKKQWAGPYVSSLYDLSLDTG 360
 QY 429 EASVLELTVNSKIENHEMLAVEPINELLRDKMRKGAVSFYINVSYSYLCAMVIFLT 488
 DB 361 EASVLELTVNSKIENHEMLAVEPINELLRDKMRKGAVSFYINVSYSYLCAMVIFLT 420
 QY 489 AAYQPLEGTPPYRTTVDYRIAGEVITLFTGVLFPTNLIKDLFMKKCPGVNSLFDGS 548
 DB 421 AAYQPLEGTPPYRTTVDYRIAGEVITLFTGVLFPTNLIKDLFMKKCPGVNSLFDGS 480
 QY 549 FOLLPIYSVAVISALYLAGIEAVLAVMVFALVGMNNAVYFTRGLKLTGYSIMIQ 608
 DB 481 FOLLPIYSVAVISALYLAGIEAVLAVMVFALVGMNNAVYFTRGLKLTGYSIMIQ 540
 QY 609 ILFDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSCRDSEFTST 668
 DB 541 ILFDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSCRDSEFTST 600
 QY 669 FLDDLFLTLTGMDLEMLSTKYPVVFIIILVTYIILFVLLNMLALMGEIVGQVSK 728

Db	601	FLDDEKFLTGMDDLFWLSTKCPVYFILLVYIIITFLVLLNMLIALNGEIVGYSK	660
QY	729	SKHWLQ 736	
Db	661	SKHWLQ 668	
RESULT 6			
ID	Q9HBA0	PRELIMINARY; PRT; 871 AA.	
AC	Q9HBA0		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Vanilloid receptor-related osmotically activated channel.		
GN	Name=VROAC;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20531888; PubMed=11081638;		
RA	Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,		
RA	Sall A., Hudspeth A.O., Friedman J.M., Heller S.;		
RT	"Vanilloid receptor-related osmotically activated channel (VR-OAC), a		
RT	candidate vertebrate osmoreceptor."		
RL	Cell 103:525-535(2000).		
DR	EMBL; AF263523; AAC28029.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005261; F:channel activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0006812; P:cation transport; IEA.		
DR	InterPro; IPR002110; ANK.		
DR	InterPro; IPR002111; Cat channel Trpl.		
DR	InterPro; IPR008996; CytoC_IL1_like.		
DR	InterPro; IPR005821; Ion trans.		
DR	InterPro; IPR004729; TRPChannel.		
DR	InterPro; IPR008347; Vanil_receptor.		
DR	InterPro; IPR008348; Vanil_receptor2.		
DR	Pfam; PF00023; Ank; 3.		
DR	Pfam; PF00520; Ion trans. 1.		
DR	PRINTS; PRO1415; ANKRYIN.		
DR	PRINTS; PRO1768; TRPVRECEPTOR.		
DR	PRINTS; PRO1769; VRL2RECEPTOR.		
DR	SMART; SM00248; ANK; 3.		
DR	TIGRFAMs; TIGR00870; trp; 1.		
DR	PROSITE; PS50086; ANK_REPEAT; 1.		
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.		
KW	ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;		
KW	Transport.		
QY	SEQUENCE 871 AA; 98265 MW; A86FB6ECC9103C19 CRC64;		
Query Match 85.6%; Score 635; DB 2; Length 871;			
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;			
Matches 735; Conservative 0;			
QY	1	MADSSSEGRAPGGEVAELPGDESGTGGGEAPPLSLIANLFRGEDGSLSPSPADASRPAPG	60
Db	1	MADSSSEGRAPGGEVAELPGDESGTGGGEAPPLSLIANLFRGEDGSLSPSPADASRPAPG	60
QY	61	GDGSPNLRMRKQGAFRKGVNPIDLLBSTLYESSVPEPKKAPMDSLTDYGYTRHSSDN	120
Db	61	GDGSPNLRMRKQGAFRKGVNPIDLLBSTLYESSVPEPKKAPMDSLTDYGYTRHSSDN	120
QY	121	KRWKRTKIIERKQSPKAPAPQPEPIILKFNRPILFDIVSRGSTDLDGLLPLLTHTKKRL	180
Db	121	KRWKRTKIIERKQSPKAPAPQPEPIILKFNRPILFDIVSRGSTDLDGLLPLLTHTKKRL	180
QY	181	TDEEFREPSNGKTLCPKALNLSNGRNDTIVYLLDIARTGNMGEFINSPPRDYYRGQT	240
Db	181	TDEEFREPSNGKTLCPKALNLSNGRNDTIVYLLDIARTGNMGEFINSPPRDYYRGQT	240

Qy	241	ALHIAIERCKHYVELLVAGQADVHQAQGRFPQPDGEGYFRFGSLPLSLAATCTOPHI	300
Db	241	ALHIAIERCKHYVELLVAGQADVHQAQGRFPQPDGEGYFRFGSLPLSLAATCTOPHI	3000
Qy	301	VNVLTEHPKKKDMRQDSRGNTVLHALVAIADNTRENTKFWYKMDLLILKKARLPDS	366
Db	301	VNVLTEHPKKKDMRQDSRGNTVLHALVAIADNTRENTKFWYKMDLLILKKARLPDS	3666
Qy	361	NIEAVIANDGSLPLMMAATGKIGIFQHIIRREVTDSDTRHLSRKFKDWAYGVPVSYLD	420
Db	361	NIEAVIANDGSLPLMMAATGKIGIFQHIIRREVTDSDTRHLSRKFKDWAYGVPVSYLD	4200
Qy	421	LSLSDCGEASVLELTVNSKIKENHHEMLAEPIINELLRDKWRKFGANSFYINVSILC	480
Db	421	LSLSDCGEASVLELTVNSKIKENHHEMLAEPIINELLRDKWRKFGANSFYINVSILC	4800
Qy	481	ANVIFLTAAVYQPLSGSTPPYPRRTVDYRLAGEVITLFTGVLFPTNKKDLFMKCCPGV	540
Db	481	ANVIFLTAAVYQPLSGSTPPYPRRTVDYRLAGEVITLFTGVLFPTNKKDLFMKCCPGV	5400
Qy	541	NSLFLIDGSGQLLYFTYSVLIVSAAIYAGIEMAYAVWPAVLGMMNALYFTRGILKTG	600
Db	541	NSLFLIDGSGQLLYFTYSVLIVSAAIYAGIEMAYAVWPAVLGMMNALYFTRGILKTG	6000
Qy	601	TVSINIOKTLFPODLREPLLVYLLFMIGYASALVSLNIPANKKVCNEODTCTVPPYBGC	660
Db	601	TVSINIOKTLFPODLREPLLVYLLFMIGYASALVSLNIPANKKVCNEODTCTVPPYBGC	6600
Qy	661	RDSEFTSFLLDLFLKLTIGMGDLEMSSTKYVVEFIILVYIILFTVLLNMLIALMSE	720
Db	661	RDSEFTSFLLDLFLKLTIGMGDLEMSSTKYVVEFIILVYIILFTVLLNMLIALMSE	7200
Qy	721	TVGVSKSKSKHMKQ 736	
Db	721	TVGVSKSKSKHMKQ 736	
RESULT 7			
ID	Q8NG64	PRELIMINARY; PRT; 811 AA.	
AC	Q8NG64;		
DT	01-OCT-2002 (Tremblrel. 22, Created)		
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	OTRCAdelta cation channel.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RE	SEQUENCE FROM N.A.		
RC	TISUB=Aortic endothelium;		
RA	Xu F., Satoh E., Iijima T.;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB073669; BAC06573.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005261; P:cation channel activity; IEA.		
DR	GO; GO:0006812; P:cation transport; IEA.		
DR	InterPro; IPR002110; ANK.		
DR	InterPro; IPR002111; Cat channel TrpL.		
DR	InterPro; IPR00896; CytoC III like.		
DR	InterPro; IPR005821; Ion trans.		
DR	InterPro; IPR008347; Vanil_receptor.		
DR	InterPro; IPR008348; Vanil_receptor2.		
DR	Pfam; PF00023; Ion trans; 1.		
DR	Pfam; PF05020; Ion trans; 3.		
DR	PRINTS; PRO1415; ANKYRIN.		
DR	PRINTS; PRO1768; TRYPRECEPTOR.		
DR	PRINTS; PRO1769; VRL2RECEPTOR.		
DR	SMART; SM00248; ANK_3.		
DR	PROSITE; PS50088; ANK_REPEAT; 1.		
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.		

RESULT 7			
Q8NG64			
ID	Q8NG64	PRELIMINARY	ERT; 811 AA.
AC	Q8NG64;		
DT	01-OCT-2002 (TREMBLrel. 22, Created)		
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
OS	Ottrc4beta cation channel.		
OC	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
NCBI	NCBI_TaxId=9606;		
NCBI	[1]		
SEQUENCE FROM N.A.			
RC	Tissue=Aortic endothelium;		
RA	Xu P, Sacho E, Iijima T;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB073669; BAC06573.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005261; P:cation channel activity; IEA.		
DR	GO; GO:0006812; P:cation transport; IEA.		
DR	InterPro; IPR002110; ANK.		
DR	InterPro; IPR002111; Cat channel TrypL.		
DR	InterPro; IPR008896; CytoK_IL1_like.		
DR	InterPro; IPR005821; Ion_chan.		
DR	InterPro; IPR008347; Vanil_receptor.		
DR	InterPro; IPR008348; Vanil_receptor2.		
DR	Pfam; PF00023; Ank; 3.		
DR	Pfam; PF00520; Ion_chan; 1.		
DR	PRINTS; PR01415; ANKYRIN.		
DR	PRINTS; PR01768; TRP_RECEPTOR.		
DR	PRINTS; PR01769; VRL2RECEPTOR.		
DR	SMART; SM00248; ANK_3.		
DR	PROSITE; PS50088; ANK_REPEAT; 1.		
DR	PROSITE; PSS0297; ANK_REPEAT_REGION; 1.		

ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
KW SEQUENCE 811 AA; 91220 MW; 3847D0FD07830781 CRC64;

Query Match 51.8%; Score 384; DB 2; Length 811;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGGRAPGGEVAFELPGDESGPGGEAFPLSLANLPGEDDSLSPSPADASRPAGP 60
DB 1 MADSSGGRAPGGEVAFELPGDESGPGGEAFPLSLANLPGEDDSLSPSPADASRPAGP 60
QY 61 GDGEPNLMTKQAFKRGVNPIDLESTLYESSVVPKKAQMDSLFDYGYTRHSSDN 120
DB 61 GDGEPNLMTKQAFKRGVNPIDLESTLYESSVVPKKAQMDSLFDYGYTRHSSDN 120
QY 121 KRWKKTIEKQPOSKAPAPQPPPLIKTPNRPILFDIYRSSTADLGLPLPLTHKKRL 180
DB 121 KRWKKTIEKQPOSKAPAPQPPPLIKTPNRPILFDIYRSSTADLGLPLPLTHKKRL 180
QY 121 KRWKKTIEKQPOSKAPAPQPPPLIKTPNRPILFDIYRSSTADLGLPLPLTHKKRL 180
DB 121 KRWKKTIEKQPOSKAPAPQPPPLIKTPNRPILFDIYRSSTADLGLPLPLTHKKRL 180
QY 181 TDEERFESTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFFINSPPEDIIYRGQT 240
DB 181 TDEERFESTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFFINSPPEDIIYRGQT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQKDEGGYFFGELPLSLAATNOPIH 300
DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQKDEGGYFFGELPLSLAATNOPIH 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHVAIDNTRENTKFTKMYDILLKCARLPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHVAIDNTRENTKFTKMYDILLKCARLPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTKIG 384
DB 361 NLEAVLNNDGSLPLMAAKTKIG 384

RESULT 8
Q9ERZ8 PRELIMINARY; PRT; 871 AA.

AC 09ERZ8; 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.
GN Name-Vracc.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=20511888; PubMed=11081638;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
cell candidate vertebrate osmoreceptor.";
RU Cell 103:525-535(2000).
DR EMBL; AF263521; AAC28027.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR008996; Cytok_IL1_Like.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; ANK_3.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01768; TRPVRECEPTOR.

DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK_3.
DR TIGRFAMs; TIGR00870; trip_1.
DR PROSITE; PS50086; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;

Query Match 24.4%; Score 181; DB 2; Length 871;
Best Local Similarity 100.0%; Pred. No. 5,9e-171;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 LITHKKRLTDEERFESTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFFINSPP 232
DB 173 LITHKKRLTDEERFESTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFFINSPP 232
QY 233 DIYRGQFALHIAIERCKHYVELLVAQADVHAQARGFPQKDEGGYFFGELPLSLA 292
DB 233 DIYRGQFALHIAIERCKHYVELLVAQADVHAQARGFPQKDEGGYFFGELPLSLA 292
QY 293 ACTNQHIVNYLTENPHKADMRQDSRGNTVLAHVAIDNTRENTKFTKMYDILLK 352
DB 293 ACTNQHIVNYLTENPHKADMRQDSRGNTVLAHVAIDNTRENTKFTKMYDILLK 352
QY 353 C 353
DB 353 C 353

RESULT 9
Q91XR5 PRELIMINARY; PRT; 803 AA.

AC 091XR5; 01-DEC-2001 (TREMELREL. 19, Created)
DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)
DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN Name=Trpv4; Synonyms=Vr12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Derst C., Schafer M.X.;
RU Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279672; AK69486.1; -
DR MGD; MGI:1226945; Trpv4.
DR GO; GO:0005262; F:calcium channel activity; IEA.
DR GO; GO:0005034; F:osmosensor activity; IEA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IEA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR008996; Cytok_IL1_Like.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; ANK_3.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK_3.
DR TIGRFAMs; TIGR00870; trip_1.
DR PROSITE; PS50086; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;

KW Transport. 803 AA; 91438 MW; 79ASBD9323300029 CRC64;
SEQUENCE

Query Match 15.1%; Score 112; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 4.5e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERCKHYVELVAQADVAHQARGFQPKDEGGYFYFGLPLSLAAGTNPHTV 301
DB 174 LHAIERCKHYVELVAQADVAHQARGFQPKDEGGYFYFGLPLSLAAGTNPHTV 233
QY 302 NYLTENPHKADMRQDSRGNTVLAHALVAADNTRENTKFTTKMYDILLKLC 353
DB 234 NYLTENPHKADMRQDSRGNTVLAHALVAADNTRENTKFTTKMYDILLKLC 285

RESULT 10

Q9EPK8 PRELIMINARY; PRT; 871 AA.

AC Q9EPK8
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transient receptor potential protein 12.
GN Name=Trpv4; Synonyms=Trp12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=20547522; PubMed=11094154;
RA Wiesenbach U., Boeding M., Freichel M., Flockert V.,
RT "Trp12, a novel Trp related protein from kidney."
RL FEBS Lett. 485:127-134(2000).
DR EMBL; AJ296078; CAC20703.1; -.
DR MGD; MGI:1926945; Trpv4.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel Trpv.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR PRINTS; PRO1769; VRL2RECEPTOR.
DR Pfam; PF00023; ANK; 3.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SO SEQUENCE 871 AA; 98026 MW; 5BAC5E33F89CEA05 CRC64;

Query Match 15.1%; Score 112; DB 2; Length 871;
Best Local Similarity 100.0%; Pred. No. 4.5e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERCKHYVELVAQADVAHQARGFQPKDEGGYFYFGLPLSLAAGTNPHTV 301
DB 242 LHAIERCKHYVELVAQADVAHQARGFQPKDEGGYFYFGLPLSLAAGTNPHTV 301
QY 302 NYLTENPHKADMRQDSRGNTVLAHALVAADNTRENTKFTTKMYDILLKLC 353

DB 302 NYLTENPHKADMRQDSRGNTVLAHALVAADNTRENTKFTTKMYDILLKLC 353

RESULT 11

Q9EQZ4 PRELIMINARY; PRT; 871 AA.

AC Q9EQZ4
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Ion channel.
GN Name=Trpv4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22692536; PubMed=12692122;
RA Suzuki M., Mizuno A., Kodaira K., Imai M.,
RT "Impaired pressure sensation in mice lacking Trpv4."
RL J. Biol. Chem. 278:22664-22668(2003).
DR EMBL; AB021875; BAA83731.2; -.
DR MGD; MGI:1926945; Trpv4.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel Trpv.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR PRINTS; PRO1769; VRL2RECEPTOR.
DR Pfam; PF00023; ANK; 3.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
KW SEQUENCE 871 AA; 98060 MW; 3285A576D32DD95 CRC64;

Query Match 15.1%; Score 112; DB 2; Length 871;
Best Local Similarity 100.0%; Pred. No. 4.5e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERCKHYVELVAQADVAHQARGFQPKDEGGYFYFGLPLSLAAGTNPHTV 301
DB 242 LHAIERCKHYVELVAQADVAHQARGFQPKDEGGYFYFGLPLSLAAGTNPHTV 301
QY 302 NYLTENPHKADMRQDSRGNTVLAHALVAADNTRENTKFTTKMYDILLKLC 353
DB 302 NYLTENPHKADMRQDSRGNTVLAHALVAADNTRENTKFTTKMYDILLKLC 353

RESULT 12

Q9ES76 PRELIMINARY; PRT; 871 AA.

AC Q9ES76
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE OTRPC4 cation channel.
GN Name=Trpv4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RX MEDLINE=20482174; PubMed=11025659;
RA Strickman R., Hartenack C., Nunnenmacher K., Schultz G., Plant T.D.;
RT "ORPDC, a nonselective cation channel that confers sensitivity to
   extracellular osmolarity";
RL Nat. Cell Biol. 2:695-702(2000).
DR EMBL, AF208026; AAG17543.1; -.
DR MGD, MGI:1926945; Trpv4.
DR GO: GO:0005262; F:calcium channel activity; IDA.
DR GO: GO:0005034; F:osmosensor activity; IDA.
DR GO: GO:0042538; P:osmosensory signaling pathway; IDA.
DR GO: GO:0004253; P:hyperosmotic salinity response; IMP.
DR GO: GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO: GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO: GO:0030103; P:vasopressin secretion; IMP.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat channel TrpL.
DR InterPro: IPR008996; CytoK IL1 like.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR004729; TRP channel.
DR InterPro: IPR008347; Vanil1_receptor.
DR InterPro: IPR008348; Vanil1_receptor2.
DR Pfam: PF00023; ANK; 3.
DR Pfam: PF00520; Ion trans; 1.
DR PRINTS: PR01768; TRPVRECEPTOR.
DR PRINTS: PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFSM; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
KM SEQUENCE 871 AA; 98069 MW; 2B28D554083F00A CRC64;
SQ

Query Match 15.1%; Score 112; DB 2; Length 873;
Best Local Similarity 100.0%; Pred. No. 4.5e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERRCKHYVELVAGADVHAQARFPQDEGGYFEGELPLSLACTNPHIV 301
DB 242 LHAIERRCKHYVELVAGADVHAQARFPQDEGGYFEGELPLSLACTNPHIV 301
QY 302 NVLTENPHKKADRRDSSRGNTVLAHVLAIDNTRENTKFTVMYDILLK 353
DB 302 NVLTENPHKKADRRDSSRGNTVLAHVLAIDNTRENTKFTVMYDILLK 353

RESULT 13
Q99RZ7 PRELIMINARY; PRT; 873 AA.
ID Q99RZ7
AC Q99RZ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.
GN Name=Trpv4; Synonyms=Vtrac;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=20531868; PubMed=11081638;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA Sali A., Hudepeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
   candidate vertebrate osmoreceptor.";
RL Cell 103:525-535(2000).
DR EMBL, AF263522; AAG28028.1; -.
DR MGD; MGI:1926945; Trpv4.

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DR GO: GO:0005262; F:calcium channel activity; IDA.
DR GO: GO:0005034; F:osmosensor activity; IDA.
DR GO: GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO: GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO: GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO: GO:0030103; P:vasopressin secretion; IMP.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat channel TrpL.
DR InterPro: IPR008996; CytoK IL1 like.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR004729; TRP channel.
DR InterPro: IPR008347; Vanil1_receptor.
DR InterPro: IPR008348; Vanil1_receptor2.
DR Pfam: PF00023; ANK; 3.
DR Pfam: PF00520; Ion trans; 1.
DR PRINTS: PR01768; TRPVRECEPTOR.
DR PRINTS: PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFSM; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
   Transport.
KM SEQUENCE 873 AA; 98596 MW; 5D87C92712B24EA CRC64;
SQ

Query Match 15.1%; Score 112; DB 2; Length 873;
Best Local Similarity 100.0%; Pred. No. 4.5e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERRCKHYVELVAGADVHAQARFPQDEGGYFEGELPLSLACTNPHIV 301
DB 242 LHAIERRCKHYVELVAGADVHAQARFPQDEGGYFEGELPLSLACTNPHIV 303
QY 302 NVLTENPHKKADRRDSSRGNTVLAHVLAIDNTRENTKFTVMYDILLK 353
DB 304 NVLTENPHKKADRRDSSRGNTVLAHVLAIDNTRENTKFTVMYDILLK 355

RESULT 14
Q99FS3 PRELIMINARY; PRT; 852 AA.
ID Q99FS3
AC Q99FS3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel protein.
GN Name=VR-OAC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Cochlea;
RX MEDLINE=20531868; PubMed=11081638;
RA Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,
RA Hudepeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
   candidate vertebrate osmoreceptor.";
RL Cell 103:525-535(2000).
DR EMBL, AF261883; AAG28026.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005261; F:calcium channel activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat channel TrpL.
DR InterPro: IPR008996; CytoK IL1 like.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR002016; Peroxidase.
DR InterPro: IPR001865; Ribosomal_S2.

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Search completed: December 2, 2004, 22:42:47
 Job time : 206 secs

DR InterPro; IPR004729; TRPchannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank_3.
 DR Pfam; PF00520; Ion_trans_1.
 DR PRINTS; PRO1415; ANKTRIN.
 DR PRINTS; PRO1768; TRPVRECEPTOR.
 DR PRINTS; PRO1769; VRL2RECEPTOR.
 DR SMART; SM00248; ANK_3.
 DR TIGRFAMs; TIGR00870; trp_1.
 DR PROSITE; PS50088; ANK_REPEAT_1.
 DR PROSITE; PS50297; ANK_REPEAT_1.
 DR PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KW Transport.
 SQ SEQUENCE 852 AA; 96197 MW; E85365D3FAD08C1 CRC64;

Query Match 9.2%; Score 68; DB 2; Length 852;
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 DB 558 EAYLAWVPALVLMGMNALYFTRLKLTGTYSIMIOKILFKDLFRPLVYLFPMTGYASA 617

QY 632 LVSLNPC 639
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 DB 618 LVSLNPC 625

RESULT 15

Q9Z182 PRELIMINARY; PRT; 528 AA.
 ID Q9Z182;
 AC Q9Z182;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Stretch-inhibitable nonselective channel (SIC).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=99156912; PubMed=10037722;
 RA Suzuki M., Sato J., Katsuwada K., Ooki G., Imai M.;
 RT "Cloning of a stretch-inhibitable nonselective cation channel.";
 RL J. Biol. Chem. 274:6330-6335 (1999).
 DR EMBL; AB015231; BA034942.2; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_TyPL.
 DR InterPro; IPR008996; CytoK_IL1_like.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR008347; Vanil_receptor.
 DR Pfam; PF00520; Ion_trans_1.
 DR PRINTS; PRO1768; TRPVRECEPTOR.
 DR SMART; SM00248; ANK_1.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 528 AA; 61017 MW; 93E4B00A6A231FD0 CRC64;

Query Match 3.8%; Score 28; DB 2; Length 528;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
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QY 709 LILNMLIALMGFTVGVSKEKSHIMKIQ 736
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 DB 366 LILNMLIALMGFTVGVSKEKSHIMKIQ 393

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OM protein - protein search, using BW model

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Title: US-10-090-215-12

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Searched: 478139 seqs, 66318000 residues

Word size: 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	16	2.2	838	4	US-09-132-316-3
7	16	2.2	838	4	US-09-667-422-9
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9	16	2.2	839	3	US-09-197-636-4
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21	14	1.9	761	4	US-09-978-303-4
22	14	1.9	764	3	US-09-235-451-36
23	14	1.9	764	4	US-09-978-303-36
24	14	1.9	889	4	US-09-132-316-2
25	11	1.5	727	3	US-09-235-451-23
26	11	1.5	727	4	US-09-978-303-23
27	10	1.3	34	4	US-09-149-476-624

28	10	1.3	57	3	US-09-235-451-15	Sequence 15, Appl
29	10	1.3	57	4	US-09-978-303-15	Sequence 15, Appl
30	9	1.2	428	4	US-09-252-991A-24452	Sequence 24452, A
31	8	1.1	84	4	US-09-248-796A-26822	Sequence 26822, A
32	8	1.1	97	3	US-08-858-207A-515	Sequence 515, App
33	8	1.1	114	4	US-09-270-767-42187	Sequence 42187, A
34	8	1.1	119	4	US-09-134-000C-4066	Sequence 4066, Ap
35	8	1.1	120	4	US-09-248-796A-24245	Sequence 24245, A
36	8	1.1	120	4	US-09-248-796A-27147	Sequence 27147, A
37	8	1.1	144	4	US-09-252-991A-16650	Sequence 16650, A
38	8	1.1	239	3	US-08-986-304-3	Sequence 3, Appl1
39	8	1.1	337	4	US-09-252-991A-26243	Sequence 26243, A
40	8	1.1	337	4	US-09-107-532A-5998	Sequence 5998, Ap
41	8	1.1	379	4	US-09-583-110-3811	Sequence 3811, A
42	8	1.1	496	4	US-09-252-991A-17357	Sequence 17357, A
43	8	1.1	570	4	US-09-252-991A-20010	Sequence 20010, A
44	8	1.1	704	4	US-09-252-991A-30631	Sequence 30631, A
45	8	1.1	725	4	US-09-350-457A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-500-123-12
; Sequence 12, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500.123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-12

Query Match Best Local Similarity 100.0%; Score 742; DB 4; Length 742;

Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MADSEGPRAAGPEVAELPGDESGTGGGEAPFLSLANTLFGEDGSLSPSPADSRPAGP	60
Db	1	MADSEGPRAAGPEVAELPGDESGTGGGEAPFLSLANTLFGEDGSLSPSPADSRPAGP	60
Qy	61	GDGPRNLRMKFGAERKGVNPIDLLSTLYESSVVPQPKAPMDSLFDVGYRHSN	120
Db	61	GDGPRNLRMKFGAERKGVNPIDLLSTLYESSVVPQPKAPMDSLFDVGYRHSN	120
Qy	121	KRMKKLIEKQSPKAPAPQPPILKFNRPILFDIVSRGTADLGLPFLTHKRL	180
Db	121	KRMKKLIEKQSPKAPAPQPPILKFNRPILFDIVSRGTADLGLPFLTHKRL	180
Qy	181	TDEFRPSTGKTLPRALINTLSGRNDTLPVLIDIERTCNMKEFTNSPRDIYRQOT	240
Db	181	TDEFRPSTGKTLPRALINTLSGRNDTLPVLIDIERTCNMKEFTNSPRDIYRQOT	240
Qy	241	ALHTAIRRCKHYELLVAQADVHAQARGFPQKDEGFFYFGELPLSLAATNOPI	300
Db	241	ALHTAIRRCKHYELLVAQADVHAQARGFPQKDEGFFYFGELPLSLAATNOPI	300
Qy	301	VNYLTENPHKADRRDROSGNTYLAHALVAIDTRENTEVYTGQYDILLKCARLPDS	360
Db	301	VNYLTENPHKADRRDROSGNTYLAHALVAIDTRENTEVYTGQYDILLKCARLPDS	360

QY 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFCKOMAYGPVYSSLYD 420
DB 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFCKOMAYGPVYSSLYD 420
QY 421 LSSLDTCGEBSVLEILVYNSKIEBRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480
DB 421 LSSLDTCGEBSVLEILVYNSKIEBRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480
QY 481 AMVIFTLTAAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKDLEFMKCKGV 540
DB 481 AMVIFTLTAAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKDLEFMKCKGV 540
QY 541 NSLFTDGSFOLLIFYISVIVISALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
DB 541 NSLFTDGSFOLLIFYISVIVISALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
QY 601 TYSIMIOKILFEDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVETPSC 660
DB 601 TYSIMIOKILFEDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVETPSC 660
QY 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVEIILVTYIILTFVLLNMLIALMGE 720
DB 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVEIILVTYIILTFVLLNMLIALMGE 720
QY 721 TVGVSKSKSKHIMKIQSGRRRL 742
DB 721 TVGVSKSKSKHIMKIQSGRRRL 742

RESULT 2

US-09-500-123-7
; Sequence 7, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Etlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-7

Query Match 85.6%; Score 635; DB 4; Length 871;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSSBGPAGGEVAELPGDESGTPGGAFLPSSIANLFBGSDGSLSPADASRPAGP 60
DB 1 MADSSBGPAGGEVAELPGDESGTPGGAFLPSSIANLFBGSDGSLSPADASRPAGP 60
QY 61 GGRPLRMKFGAARPKGVNPIIDLESTLYESSVVPCKAPMDSLFGYGYRRHSSDN 120
DB 61 GGRPLRMKFGAARPKGVNPIIDLESTLYESSVVPCKAPMDSLFGYGYRRHSSDN 120
QY 121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180
DB 121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180
QY 181 TDEBFEPESTGTCPLKALINLSNGRNDITPVLDIAERTGNMREPTNSPPFDIYYRGOT 240
DB 181 TDEBFEPESTGTCPLKALINLSNGRNDITPVLDIAERTGNMREPTNSPPFDIYYRGOT 240
QY 241 AHHIAIERCKHYVELLVAGADVHAQARGFPQKDEGGYFYFGLPLSLAATNOPIH 300
DB 241 AHHIAIERCKHYVELLVAGADVHAQARGFPQKDEGGYFYFGLPLSLAATNOPIH 300

DB 241 AHHIAIERCKHYVELLVAGADVHAQARGFPQKDEGGYFYFGLPLSLAATNOPIH 300
QY 301 VNYLTENPHKTAADMRRQDSRGNTVLHAIVALADNTRNTKEVTKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKTAADMRRQDSRGNTVLHAIVALADNTRNTKEVTKMYDILLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFCKOMAYGPVYSSLYD 420
DB 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFCKOMAYGPVYSSLYD 420
QY 421 LSSLDTCGEBSVLEILVYNSKIEBRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480
DB 421 LSSLDTCGEBSVLEILVYNSKIEBRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480
QY 481 AMVIFTLTAAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKDLEFMKCKGV 540
DB 481 AMVIFTLTAAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKDLEFMKCKGV 540
QY 541 NSLFTDGSFOLLIFYISVIVISALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
DB 541 NSLFTDGSFOLLIFYISVIVISALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
QY 601 TYSIMIOKILFEDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVETPSC 660
DB 601 TYSIMIOKILFEDLFRFLVYLFLMIGYASALVSLNFCAMKVCNEDQNTCTVETPSC 660
QY 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVEIILVTYIILTFVLLNMLIALMGE 720
DB 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVEIILVTYIILTFVLLNMLIALMGE 720
QY 721 TVGVSKSKSKHIMKIQ 736
DB 721 TVGVSKSKSKHIMKIQ 736

RESULT 3

US-09-500-123-9
; Sequence 9, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Etlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-9

Query Match 51.6%; Score 383; DB 4; Length 811;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSBGPAGGEVAELPGDESGTPGGAFLPSSIANLFBGSDGSLSPADASRPAGP 60
DB 1 MADSSBGPAGGEVAELPGDESGTPGGAFLPSSIANLFBGSDGSLSPADASRPAGP 60
QY 61 GGRPLRMKFGAARPKGVNPIIDLESTLYESSVVPCKAPMDSLFGYGYRRHSSDN 120
DB 61 GGRPLRMKFGAARPKGVNPIIDLESTLYESSVVPCKAPMDSLFGYGYRRHSSDN 120
QY 121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180
DB 121 KMRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180

QY 181 TDEERESTGTCPLKALINLSGRNDTIPVLIDIAERTGNMREFFINSPPREDIYRQQT 240
| | | | |
Db 181 TDEERESTGTCPLKALINLSGRNDTIPVLIDIAERTGNMREFFINSPPREDIYRQQT 240
QY 241 ALHIAIERCKHYVLLVAOGADYVAOARGRFPQKDGXYFYFGEPLSLAAGTNOPI 300
| | | | |
Db 241 ALHIAIERCKHYVLLVAOGADYVAOARGRFPQKDGXYFYFGEPLSLAAGTNOPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNTRENTKTYKMYDLLLKCARLFPDS 360
| | | | |
Db 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNTRENTKTYKMYDLLLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTGKI 383
| | | | |
Db 361 NLEAVLNNDGSLPLMAAKTGKI 383

RESULT 4
US-09-667-422-5
; Sequence 5, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; EARLIER FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (434)..(455)
; OTHER INFORMATION: TML
; NAME/KEY: TRANSMEM
; LOCATION: (480)..(495)
; OTHER INFORMATION: TML
US-09-667-422-5

Query Match
Best Local Similarity 2.2%; Score 16; DB 4; Length 511;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLAAGTNO 297
| | | | |
Db 246 FYFGEPLSLAAGTNO 261

RESULT 5
US-09-235-451-2
; Sequence 2, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; EARLIER FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 838

; TYPE: PRT
; ORGANISM: R. rattus
US-09-235-451-2

Query Match
Best Local Similarity 2.2%; Score 16; DB 3; Length 838;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLAAGTNO 297
| | | | |
Db 245 FYFGEPLSLAAGTNO 260

RESULT 6
US-09-132-316-3
; Sequence 3, Application US/09132316B
; Patent No. 6444440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1488.110000
; CURRENT APPLICATION NUMBER: US/09/132,316B
; EARLIER FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-132-316-3

Query Match
Best Local Similarity 2.2%; Score 16; DB 4; Length 838;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLAAGTNO 297
| | | | |
Db 245 FYFGEPLSLAAGTNO 260

RESULT 7
US-09-667-422-9
; Sequence 9, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; EARLIER FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus sp.
; PUBLICATION INFORMATION:
; AUTHORS: Caterina, Michael J.
; AUTHORS: Schumacher, Mark A.
; AUTHORS: Tomihaga, Makoto
; AUTHORS: Rosen, Tobias A.
; TITLE: The capsaicin receptor: a heat-activated ion channel in
; JOURNAL: Nature
; VOLUME: 389
; PAGES: 816-824
; DATE: 1997

US-09-667-422-9

Query Match 2.2% Score 16; DB 4; Length 838;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLACTNQ 297
DB 245 FYFGELPLSLACTNQ 260

RESULT 8

US-09-978-303-2
Sequence 2, Application US/09978303

Patent No. 6790629
GENERAL INFORMATION:
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
TITLE OF INVENTION: Nucleic acid sequences encoding
TITLE OF INVENTION: Capsaicin receptor and capsaicin receptor-related
TITLE OF INVENTION: polypeptides and uses thereof
FILE REFERENCE: UCA1084CON
CURRENT APPLICATION NUMBER: US/09/978,303
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 838
TYPE: PRT
ORGANISM: R. rattus
US-09-978-303-2

Query Match 2.2% Score 16; DB 4; Length 838;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLACTNQ 297
DB 245 FYFGELPLSLACTNQ 260

RESULT 9

US-09-197-636-2
Sequence 2, Application US/09197636

Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636

FILING DATE: 23-NOV-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UK 9805137.8

FILING DATE: 12-MAR-1998

APPLICATION NUMBER: UK 9815791.0

FILING DATE: 21-JUL-1998

APPLICATION NUMBER: UK 9819278.4

FILING DATE: 03-SEP-1998

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GP-30075

TELECOMMUNICATION INFORMATION:

TELEPHONE: 601-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 839 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-197-636-2

Query Match 2.2% Score 16; DB 3; Length 839;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLACTNQ 297
DB 246 FYFGELPLSLACTNQ 261

RESULT 10

US-09-197-636-4
Sequence 4, Application US/09197636

Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30075

TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-197-636-4

Query Match 2.2%; Score 16; DB 3; Length 839;
Best Local Similarity 100.0%; Pred. No. 4,7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297
Db 246 FYFGELPLSLAQTQ 261

RESULT 11
US-09-197-636-8
Sequence 8, Application US/09197636
Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-197-636-8

Query Match 2.2%; Score 16; DB 3; Length 839;
Best Local Similarity 100.0%; Pred. No. 4,7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297
Db 246 FYFGELPLSLAQTQ 261

RESULT 12
US-09-235-451-34
Sequence 34, Application US/09235451
GENERAL INFORMATION:
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
FILE REFERENCE: 9076/084CIP
CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 34
LENGTH: 839
TYPE: PRT
ORGANISM: Homo sapiens
US-09-235-451-34

Query Match 2.2%; Score 16; DB 3; Length 839;
Best Local Similarity 100.0%; Pred. No. 4,7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297
Db 246 FYFGELPLSLAQTQ 261

RESULT 13
US-09-533-220A-2
Sequence 2, Application US/09533220A
Patent No. 6406908
GENERAL INFORMATION:
APPLICANT: McIntyre, Peter
APPLICANT: James, Iain Fraser
TITLE OF INVENTION: Human Vanilloid Receptor
FILE REFERENCE: 4-30875A
CURRENT APPLICATION NUMBER: US/09/533,220A
CURRENT FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 1.30
SEQ ID NO 2
LENGTH: 839
TYPE: PRT
ORGANISM: Homo sapiens
US-09-533-220A-2

Query Match 2.2%; Score 16; DB 4; Length 839;
Best Local Similarity 100.0%; Pred. No. 4,7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297
Db 246 FYFGELPLSLAQTQ 261

RESULT 14

US-09-667-422-4
; Sequence 4, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (434)..(455)
; OTHER INFORMATION: TM1
; NAME/KEY: TRANSMEM
; LOCATION: (480)..(495)
; OTHER INFORMATION: TM2
; NAME/KEY: TRANSMEM
; LOCATION: (510)..(530)
; OTHER INFORMATION: TM3
; NAME/KEY: TRANSMEM
; LOCATION: (543)..(569)
; OTHER INFORMATION: TM4
; NAME/KEY: TRANSMEM
; LOCATION: (577)..(596)
; OTHER INFORMATION: TMS
; NAME/KEY: TRANSMEM
; LOCATION: (656)..(684)
; OTHER INFORMATION: TM6
; US-09-667-422-4

Query Match 2.2%; Score 16; DB 4; Length 839;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLAQTNO 297
Db 246 FYFGELPLSLAQTNO 261

RESULT 15

US-09-978-303-34
; Sequence 34, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCA1084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-978-303-34

Query Match 2.2%; Score 16; DB 4; Length 839;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLAQTNO 297
Db 246 FYFGELPLSLAQTNO 261

Search completed: December 2, 2004, 22:55:04
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:45:47 ; Search time 147 Seconds

(without alignments)
1800.098 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 742

Sequence: 1 MADSSGPRAGPGVAVLPG.....GVSKSKHKLQSGRRRL 742

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1582122 seqs, 35623098 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Published Applications AA:*

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- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	742	100.0	742	14	US-10-090-215-12 Sequence 12, Appl
2	736	99.2	831	15	US-10-342-844-76 Sequence 76, Appl
3	736	99.2	870	16	US-10-761-065-2 Sequence 2, Appl
4	736	99.2	871	10	US-09-870-090-2 Sequence 2, Appl
5	736	99.2	871	14	US-10-000-823-7 Sequence 7, Appl
6	736	99.2	871	14	US-10-171-319-17 Sequence 17, Appl
7	736	99.2	871	15	US-10-342-844-54 Sequence 54, Appl
8	736	99.2	871	15	US-10-342-844-58 Sequence 58, Appl
9	736	99.2	871	15	US-10-342-844-78 Sequence 78, Appl
10	736	99.2	871	17	US-10-415-570A-2 Sequence 2, Appl
11	668	90.0	803	15	US-10-342-844-56 Sequence 56, Appl
12	635	85.6	871	14	US-10-027-828-2 Sequence 2, Appl
13	635	85.6	871	14	US-10-027-828-4 Sequence 4, Appl

14	635	85.6	871	14	US-10-090-215-7	Sequence 7, Appl
15	635	85.6	871	15	US-10-342-844-60	Sequence 60, Appl
16	567	76.4	792	9	US-09-764-367A-2	Sequence 2, Appl
17	504	67.9	963	10	US-09-932-165-1477	Sequence 1477, Ap
18	452	60.9	602	10	US-09-870-090-4	Sequence 4, Appl
19	452	60.9	602	16	US-10-761-065-4	Sequence 4, Appl
20	449	60.5	625	10	US-09-932-165-1507	Sequence 1507, Ap
21	396	53.4	871	14	US-10-227-855A-3	Sequence 3, Appl
22	383	51.6	811	14	US-10-090-215-9	Sequence 9, Appl
23	365	49.2	803	9	US-09-764-367A-8	Sequence 8, Appl
24	362	48.8	559	14	US-10-297-022-10	Sequence 10, Appl
25	316	42.6	743	9	US-09-764-367A-11	Sequence 11, Appl
26	292	39.4	734	9	US-09-764-367A-4	Sequence 4, Appl
27	222	29.9	625	10	US-09-932-165-1506	Sequence 1506, Ap
28	202	27.2	498	14	US-10-168-651-2	Sequence 2, Appl
29	181	24.4	830	14	US-10-027-828-6	Sequence 6, Appl
30	181	24.4	871	14	US-10-027-828-8	Sequence 8, Appl
31	181	24.4	871	14	US-10-027-828-9	Sequence 9, Appl
32	181	24.4	871	14	US-10-027-828-10	Sequence 10, Appl
33	181	24.4	871	14	US-10-027-828-11	Sequence 11, Appl
34	181	24.4	871	14	US-10-342-844-66	Sequence 66, Appl
35	163	22.0	166	15	US-10-276-774-1571	Sequence 1571, Ap
36	112	15.1	803	15	US-10-342-844-62	Sequence 62, Appl
37	112	15.1	870	14	US-10-027-828-13	Sequence 13, Appl
38	112	15.1	871	14	US-10-227-855A-1	Sequence 1, Appl
39	112	15.1	871	14	US-10-171-319-14	Sequence 14, Appl
40	112	15.1	871	15	US-10-342-844-80	Sequence 80, Appl
41	112	15.1	871	15	US-10-342-844-84	Sequence 84, Appl
42	112	15.1	873	15	US-10-342-844-64	Sequence 64, Appl
43	87	11.7	420	14	US-10-027-828-7	Sequence 7, Appl
44	87	11.7	461	14	US-10-027-828-5	Sequence 5, Appl
45	68	9.2	852	14	US-10-027-828-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-10-090-215-12
; Sequence 12, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/090,215
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-215-12

Query Match 100.0%; Score 742; DB 14; Length 742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MADSSGPRAGPGVAVLPGDEGTGGEAPPLISLANTFEGGDSISPSPADSRPAGP	60
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Db	61	GDGPNLRMFGQAFRGVPPIDILSTYESSVVPQPKAPMDSLFDYGTYHHSSDN	120
Qy	121	KRAKKTIHQPSGPKAPAPPPILKVFNNPILFDIVSRGSTDADGLLPLTLTKKRL	180
Db	121	KRAKKTIHQPSGPKAPAPPPILKVFNNPILFDIVSRGSTDADGLLPLTLTKKRL	180

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Db 181 TDEEERESTGKTCIPKALMLNSGRNDTIIPVLDIAERTGMREFINSPFEDIYYRGQT 240
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Db 241 ALHIAIERCKHYVELLVAQGDVHAQARGFPQKDEGCGYFPGELPLSLAAGTNOPIH 300
Qy 301 VNYLTENPHKADMRQDSRGNTVHALVALADNRENTKFTKMYDILLKCARLFPDS 360
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Db 421 LSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480
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Db 661 RDSEFSTFLDLPLFLITGMDLEMLSTKYPVVFIIILVYIIILTFVLLNMLTALMGE 720
Qy 721 TVGVSKESKHIWKLOSGRRRL 742
Db 721 TVGVSKESKHIWKLOSGRRRL 742

RESULT 2
US-10-342-844-76
; Sequence 76, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Staudeman, Kenneth
; APPLICANT: Velicelebi, G'n, I
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; FILE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 831
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 804, 816
; OTHER INFORMATION: Xaa = Any Amino Acid
; PUBLICATION INFORMATION:
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; DATABASE ACCESSION NUMBER: Genbank XP_012261
; DATABASE ENTRY DATE: 2001-10-16
US-10-342-844-76
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Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 736; Conservative 0;

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Db 1 MADSEGRAPGEVAFELPGDESGTPGGEAFPLSLIANLFEDEDSLSPSPADASRPAGP 60
Qy 61 GDGRNLMKFGQAFKGVNPIDILESTLYBSSVYVPGKAPMDSLFDYGYRHHSSDN 120
Db 61 GDGRNLMKFGQAFKGVNPIDILESTLYBSSVYVPGKAPMDSLFDYGYRHHSSDN 120
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Db 121 KRWKKIIIEKQPOSEKAPAPPPILKVFNRPILEDIYVRSGSTADLDGLPFLTHKKRL 180
Qy 181 TDEEERESTGKTCIPKALMLNSGRNDTIIPVLDIAERTGMREFINSPFEDIYYRGQT 240
Db 181 TDEEERESTGKTCIPKALMLNSGRNDTIIPVLDIAERTGMREFINSPFEDIYYRGQT 240
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Db 241 ALHIAIERCKHYVELLVAQGDVHAQARGFPQKDEGCGYFPGELPLSLAAGTNOPIH 300
Qy 301 VNYLTENPHKADMRQDSRGNTVHALVALADNRENTKFTKMYDILLKCARLFPDS 360
Db 301 VNYLTENPHKADMRQDSRGNTVHALVALADNRENTKFTKMYDILLKCARLFPDS 360
Qy 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDETRHLSRKFQKMAVGYVSSLYD 420
Db 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDETRHLSRKFQKMAVGYVSSLYD 420
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Db 421 LSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480
Qy 481 AMVITLTAAYOPLRGTPPYRTVDYLRLAGEVITLFTGVLFPTNKKDLFMKKCGV 540
Db 481 AMVITLTAAYOPLRGTPPYRTVDYLRLAGEVITLFTGVLFPTNKKDLFMKKCGV 540
Qy 541 NSLFDGSGFOLLFYYSVLVIVSAALYLAGIBAYLAVVWFALVIGMNNALYFTRGKLTG 600
Db 541 NSLFDGSGFOLLFYYSVLVIVSAALYLAGIBAYLAVVWFALVIGMNNALYFTRGKLTG 600
Qy 601 TYSIMIQKILFQDLRFLLVYLLFMIGYASALVSLNPCANMKVCNEQTNCTVPTYPSC 660
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Db 661 RDSEFSTFLDLPLFLITGMDLEMLSTKYPVVFIIILVYIIILTFVLLNMLTALMGE 720
Qy 721 TVGVSKESKHIWKLO 736
Db 721 TVGVSKESKHIWKLO 736

RESULT 3
US-10-761-065-2
; Sequence 2, Application US/10761065
; Publication No. US20040137573A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; APPLICANT: Katsuhiko Shinojo
; APPLICANT: Hikaru Yabuuchi
; TITLE OF INVENTION: Human Vanilloid Receptor-like Proteins
; FILE REFERENCE: PC9979ADAM
; CURRENT APPLICATION NUMBER: US/10/761,065
; CURRENT FILING DATE: 2004-01-20
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; PRIOR APPLICATION NUMBER: US/09/870,090A
 ; PRIOR FILING DATE: 2001-05-30
 ; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins
 ; FILE REFERENCE: PC9979A
 ; CURRENT APPLICATION NUMBER: US/09/870,090
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 870
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-761-065-2

Query Match 99.2%; Score 736; DB 16; Length 870;
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DB	181	TDEERREPGTKTCIPKALMLNSGRNDTIVLADIAERTGNMREFINSPPFDIYYRGOT	240
QY	241	ALHIAIERCKHYVELVAQADVAHAQARGFPQKDEGGYFFGELPLSLAAGTNOPI	300
DB	241	ALHIAIERCKHYVELVAQADVAHAQARGFPQKDEGGYFFGELPLSLAAGTNOPI	300
QY	301	VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS	360
DB	301	VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS	360
QY	361	NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXDMAGPVYSSLYD	420
DB	361	NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXDMAGPVYSSLYD	420
QY	421	LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYL	480
DB	421	LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYL	480
QY	481	AMVIFTLTAAVYQPLEGTPPYRTVDYLRLAGEVITLFTGVLPFTNIKDLFMKCPGV	540
DB	481	AMVIFTLTAAVYQPLEGTPPYRTVDYLRLAGEVITLFTGVLPFTNIKDLFMKCPGV	540
QY	541	NSLFDGSGFQLLYFYSLVIVSALYAGIEAYLAVWVAFVLCGMNALYFTRGLKLTG	600
DB	541	NSLFDGSGFQLLYFYSLVIVSALYAGIEAYLAVWVAFVLCGMNALYFTRGLKLTG	600
QY	601	TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNLCANMKVCNEQDQNTCTVPTPSC	660
DB	601	TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNLCANMKVCNEQDQNTCTVPTPSC	660
QY	661	RDSEFTSTFLDLDFKLTIGMGDLEMLSTKTPVVFIIILVTYIILTFVLLNMLTALMGE	720
DB	661	RDSEFTSTFLDLDFKLTIGMGDLEMLSTKTPVVFIIILVTYIILTFVLLNMLTALMGE	720
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DB	721	TVGVSKSKHIMKQ 736	

RESULT 4
 US-09-870-090-2
 ; Sequence 2, Application US/09870090
 ; Publication No. US20030017527A1

; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Product Inc.
 ; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins
 ; FILE REFERENCE: PC9979A
 ; CURRENT APPLICATION NUMBER: US/09/870,090
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-870-090-2

Query Match 99.2%; Score 736; DB 10; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MADSEGRAPGGEVAAELPGDESGTPGGEAPPLSLANLFGEDGSLSPSPADARPPAGP	60
QY	61	GDGRPNLMKFGAARFKGVNPIDLLSESTLYESSVVPKKAAMDLSFDYGYRHHSSDN	120
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QY	121	KRWKRIIEKOPQSPKAPAPPPPLIKVFNRPILFDIVSRGSTADLDGLPPLTHKKRL	180
DB	121	KRWKRIIEKOPQSPKAPAPPPPLIKVFNRPILFDIVSRGSTADLDGLPPLTHKKRL	180
QY	181	TDEERREPGTKTCIPKALMLNSGRNDTIVLADIAERTGNMREFINSPPFDIYYRGOT	240
DB	181	TDEERREPGTKTCIPKALMLNSGRNDTIVLADIAERTGNMREFINSPPFDIYYRGOT	240
QY	241	ALHIAIERCKHYVELVAQADVAHAQARGFPQKDEGGYFFGELPLSLAAGTNOPI	300
DB	241	ALHIAIERCKHYVELVAQADVAHAQARGFPQKDEGGYFFGELPLSLAAGTNOPI	300
QY	301	VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS	360
DB	301	VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS	360
QY	361	NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXDMAGPVYSSLYD	420
DB	361	NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXDMAGPVYSSLYD	420
QY	421	LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYL	480
DB	421	LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYL	480
QY	481	AMVIFTLTAAVYQPLEGTPPYRTVDYLRLAGEVITLFTGVLPFTNIKDLFMKCPGV	540
DB	481	AMVIFTLTAAVYQPLEGTPPYRTVDYLRLAGEVITLFTGVLPFTNIKDLFMKCPGV	540
QY	541	NSLFDGSGFQLLYFYSLVIVSALYAGIEAYLAVWVAFVLCGMNALYFTRGLKLTG	600
DB	541	NSLFDGSGFQLLYFYSLVIVSALYAGIEAYLAVWVAFVLCGMNALYFTRGLKLTG	600
QY	601	TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNLCANMKVCNEQDQNTCTVPTPSC	660
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QY	721	TVGVSKSKHIMKQ 736	
DB	721	TVGVSKSKHIMKQ 736	

RESULT 5
US-10-000-823-7
; Sequence 7, Application US/10000823
; Publication No. US20030027164A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NO
; FILE REFERENCE: DOI109NP
; CURRENT APPLICATION NUMBER: US/10/000,823
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/250,587
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-823-7

Query Match 99.2%; Score 736; DB 14; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGEVAELPGDESGTPGGEAPFLSIANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGEVAELPGDESGTPGGEAPFLSIANLFEGEDGSLSPSPADASRPAGP 60
QY 61 GGRGNLMMKFGARFKVGNPNDIDLESTLYESSVVPQKAPMDSLPDYGYRRHSSN 120
DB 61 GGRGNLMMKFGARFKVGNPNDIDLESTLYESSVVPQKAPMDSLPDYGYRRHSSN 120
QY 121 KMRKKTIEKOPQSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
DB 121 KMRKKTIEKOPQSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
QY 121 TDEEFREBPGTKCLPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240
DB 121 TDEEFREBPGTKCLPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240
QY 181 TDEEFREBPGTKCLPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240
DB 181 TDEEFREBPGTKCLPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240
QY 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQKDEGGYVFGELPLSLAACNQHPI 300
DB 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQKDEGGYVFGELPLSLAACNQHPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIDNTRNTKFTYKAYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIDNTRNTKFTYKAYDILLKCARLFPDS 360
QY 361 NIEAVLANDGSLPLMAAKTGKIGIFOHIIIRREVDEDTRHLSRKFKOMAYGPVYSLYD 420
DB 361 NIEAVLANDGSLPLMAAKTGKIGIFOHIIIRREVDEDTRHLSRKFKOMAYGPVYSLYD 420
QY 421 LSSLTGCEBAVSELIVYNSKIENRHEMLAVEPINELIRDKMRKFGAVSFIIYVSYLC 480
DB 421 LSSLTGCEBAVSELIVYNSKIENRHEMLAVEPINELIRDKMRKFGAVSFIIYVSYLC 480
QY 481 AMVIFTLAAYOPLGTEPPYPRYRTVDYLRLAGEVITLFTGYLFFETNIKDLFMKCKGV 540
DB 481 AMVIFTLAAYOPLGTEPPYPRYRTVDYLRLAGEVITLFTGYLFFETNIKDLFMKCKGV 540
QY 541 NSLFLDGSQQLLYFYISVLYVSAAALYAGIAYLAVMFAYLVGMNALYTRGLKLTG 600
DB 541 NSLFLDGSQQLLYFYISVLYVSAAALYAGIAYLAVMFAYLVGMNALYTRGLKLTG 600
QY 601 TYSIMIQKILFQDLRFLVLLFMIGYASALVSLNPCANKVCEQDQNTCTVPTYSBC 660
DB 601 TYSIMIQKILFQDLRFLVLLFMIGYASALVSLNPCANKVCEQDQNTCTVPTYSBC 660
QY 661 RDESEFSTFLDLFLKLTIGMDLEMLSTKYEVVEIILLVYIILFVLLNMLTALMGE 720
DB 661 RDESEFSTFLDLFLKLTIGMDLEMLSTKYEVVEIILLVYIILFVLLNMLTALMGE 720

QY 721 TVGQVSKSKHIMKIQ 736
DB 721 TVGQVSKSKHIMKIQ 736

RESULT 6
US-10-171-319-17
; Sequence 17, Application US/10171319
; Publication No. US20030157633A1
; GENERAL INFORMATION:
; APPLICANT: Arden Patapoutian
; APPLICANT: Andrea Peller
; APPLICANT: Peter McIntyre
; APPLICANT: Stuart Bevan
; APPLICANT: Chuanzheng Song
; APPLICANT: Pamosh Ganju
; TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS
; FILE REFERENCE: 4-32048A
; CURRENT APPLICATION NUMBER: US/10/171,319
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/297,835
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/351,238
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/352,914
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/357,161
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/381,086
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/381,739
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FaetsEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-319-17

Query Match 99.2%; Score 736; DB 14; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGEVAELPGDESGTPGGEAPFLSIANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGEVAELPGDESGTPGGEAPFLSIANLFEGEDGSLSPSPADASRPAGP 60
QY 61 GGRGNLMMKFGARFKVGNPNDIDLESTLYESSVVPQKAPMDSLPDYGYRRHSSN 120
DB 61 GGRGNLMMKFGARFKVGNPNDIDLESTLYESSVVPQKAPMDSLPDYGYRRHSSN 120
QY 121 KMRKKTIEKOPQSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
DB 121 KMRKKTIEKOPQSKAPAPPPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180
QY 181 TDEEFREBPGTKCLPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240
DB 181 TDEEFREBPGTKCLPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240
QY 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQKDEGGYVFGELPLSLAACNQHPI 300
DB 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQKDEGGYVFGELPLSLAACNQHPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIDNTRNTKFTYKAYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIDNTRNTKFTYKAYDILLKCARLFPDS 360
QY 361 NIEAVLANDGSLPLMAAKTGKIGIFOHIIIRREVDEDTRHLSRKFKOMAYGPVYSLYD 420
DB 361 NIEAVLANDGSLPLMAAKTGKIGIFOHIIIRREVDEDTRHLSRKFKOMAYGPVYSLYD 420

QY 421 LSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480
 Db 421 LSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480
 QY 481 AMVIFTLTAYYQPLEGPPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCKPGV 540
 Db 481 AMVIFTLTAYYQPLEGPPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCKPGV 540
 QY 541 NSLFDGSPOLLIFYSVLYVSAALYAGIEAVYAVWVAVLVGMNALVFTRGKLTG 600
 Db 541 NSLFDGSPOLLIFYSVLYVSAALYAGIEAVYAVWVAVLVGMNALVFTRGKLTG 600
 QY 601 TYSIMIOKILFKDIFRFLVYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660
 Db 601 TYSIMIOKILFKDIFRFLVYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660
 QY 661 RDSEFSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720
 Db 661 RDSEFSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720
 QY 721 TVGVSKSKHIMKIQ 736
 Db 721 TVGVSKSKHIMKIQ 736

RESULT 7

US-10-342-844-54
 ; Sequence 54, Application US/10342844
 ; Publication No. US20040009537A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roos, Jack
 ; APPLICANT: Stauderman, Kenneth
 ; APPLICANT: Velicelēbi, G'n.1
 ; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
 ; FILE REFERENCE: 37481-3307
 ; CURRENT APPLICATION NUMBER: US/10/342, 844
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: US 60/347,459
 ; PRIOR FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: US 60/401,171
 ; PRIOR FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: US 60/405,678
 ; PRIOR FILING DATE: 2002-08-20
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 54
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: Genbank XP_0271181
 ; DATABASE ENTRY DATE: 2002-09-01
 US-10-342-844-54

Query Match 99.2%; Score 736; DB 15; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSBPRAGPGEVVALPGDESGTGGGAFFPLSLANTFEGFGSLSPSPADSRAPG 60
 Db 1 MADSSBPRAGPGEVVALPGDESGTGGGAFFPLSLANTFEGFGSLSPSPADSRAPG 60
 QY 61 GDRPNLRMKFOGAFRGVNPIDILLESSTYESSVVPKPAWDSLFYGYTHHSSDN 120
 Db 61 GDRPNLRMKFOGAFRGVNPIDILLESSTYESSVVPKPAWDSLFYGYTHHSSDN 120
 QY 121 KRRRKTIKPOSPKAPAPQPPPIIKVFNRPILFDIVSGSTADLDGLLPFLITHKRL 180
 Db 121 KRRRKTIKPOSPKAPAPQPPPIIKVFNRPILFDIVSGSTADLDGLLPFLITHKRL 180
 QY 181 TDEFPSTGKTCLPALINLSGRNDTLPVLDIIFERGNMREFINSFPRDIYYRGOT 240
 Db 181 TDEFPSTGKTCLPALINLSGRNDTLPVLDIIFERGNMREFINSFPRDIYYRGOT 240

Db 181 TDEFPSTGKTCLPALINLSGRNDTLPVLDIIFERGNMREFINSFPRDIYYRGOT 240
 QY 241 ALHIAIERCKHVVYELVAOGADVYAOARGPPOPKDEGGYFYGELSLIACTNPHI 300
 Db 241 ALHIAIERCKHVVYELVAOGADVYAOARGPPOPKDEGGYFYGELSLIACTNPHI 300
 QY 301 VNYLTENPHKXADMRQDSRGNTVLAHALVAIADNTRENTKVTYKYDYDLLKCARLPDS 360
 Db 301 VNYLTENPHKXADMRQDSRGNTVLAHALVAIADNTRENTKVTYKYDYDLLKCARLPDS 360
 QY 361 NLEAVLANDGSLPLMAAKTKIGIFQHIIRREVTDEDTRIHSRFXKDMAGPVVSYLD 420
 Db 361 NLEAVLANDGSLPLMAAKTKIGIFQHIIRREVTDEDTRIHSRFXKDMAGPVVSYLD 420
 QY 421 LSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480
 Db 421 LSLDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480
 QY 481 AMVIFTLTAYYQPLEGPPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCKPGV 540
 Db 481 AMVIFTLTAYYQPLEGPPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCKPGV 540
 QY 541 NSLFDGSPOLLIFYSVLYVSAALYAGIEAVYAVWVAVLVGMNALVFTRGKLTG 600
 Db 541 NSLFDGSPOLLIFYSVLYVSAALYAGIEAVYAVWVAVLVGMNALVFTRGKLTG 600
 QY 601 TYSIMIOKILFKDIFRFLVYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660
 Db 601 TYSIMIOKILFKDIFRFLVYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660
 QY 661 RDSEFSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720
 Db 661 RDSEFSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720
 QY 721 TVGVSKSKHIMKIQ 736
 Db 721 TVGVSKSKHIMKIQ 736

RESULT 8

US-10-342-844-58
 ; Sequence 58, Application US/10342844
 ; Publication No. US20040009537A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roos, Jack
 ; APPLICANT: Stauderman, Kenneth
 ; APPLICANT: Velicelēbi, G'n.1
 ; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
 ; FILE REFERENCE: 37481-3307
 ; CURRENT APPLICATION NUMBER: US/10/342, 844
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: US 60/347,459
 ; PRIOR FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: US 60/401,171
 ; PRIOR FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: US 60/405,678
 ; PRIOR FILING DATE: 2002-08-20
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 58
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: Genbank BAB69040
 ; DATABASE ENTRY DATE: 2001-10-02
 US-10-342-844-58

Query Match 99.2%; Score 736; DB 15; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSEGRAPGGEVAVELPGDESGTGGGEAPPLSLANLFEDEGSLSPSPADASRPAGP 60
DB 1 MADSEGRAPGGEVAVELPGDESGTGGGEAPPLSLANLFEDEGSLSPSPADASRPAGP 60
QY 61 GDGRPNLMMKQGAARFKNVPPIDLESTLYESSVVPCKAPMDSLFDYGYTHHSSDN 120
DB 61 GDGRPNLMMKQGAARFKNVPPIDLESTLYESSVVPCKAPMDSLFDYGYTHHSSDN 120
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
QY 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
DB 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
QY 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
DB 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
QY 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
QY 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
QY 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
DB 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
QY 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
DB 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
QY 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
QY 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
QY 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
DB 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
QY 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
DB 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
QY 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
DB 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
QY 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
DB 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
QY 721 TVGVSKSKSHIWKQ 736
DB 721 TVGVSKSKSHIWKQ 736
QY 721 TVGVSKSKSHIWKQ 736
DB 721 TVGVSKSKSHIWKQ 736

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Genbank AAC16127
; DATABASE ENTRY DATE: 2000-09-26
; US-10-342-844-78

Query Match          99.2%; Score 736; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGRAPGGEVAVELPGDESGTGGGEAPPLSLANLFEDEGSLSPSPADASRPAGP 60
DB 1 MADSEGRAPGGEVAVELPGDESGTGGGEAPPLSLANLFEDEGSLSPSPADASRPAGP 60
QY 61 GDGRPNLMMKQGAARFKNVPPIDLESTLYESSVVPCKAPMDSLFDYGYTHHSSDN 120
DB 61 GDGRPNLMMKQGAARFKNVPPIDLESTLYESSVVPCKAPMDSLFDYGYTHHSSDN 120
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELTHKRL 180
QY 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
DB 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
QY 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
DB 181 TDEEFREPGTGTCLPKALMLNSGRNDTIPYLLDIAERTGMREFINSPPFDIYYRGQT 240
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGGYFGEPLPLSLACTIONS 300
QY 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
QY 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKFTVTKMYDILLKCARLFPDS 360
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDETRHLSRKFKOMAYGPVSSLYD 420
QY 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
DB 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
QY 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
DB 421 LSSLDTCGEASVLELIVNSKIENRHEMLAVEPINELRDKMRFGAVSFYINVSYL 480
QY 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
QY 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTPEPYRTVDYLRAGEVITLFTGVLPFTINIKDLFMKCPGV 540
QY 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
DB 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
QY 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
DB 541 NSLFTDGSFOLLFTYISVLYISAAIYLAGIYAYLAWVWFAVLGMNMLYFTRGLKLTG 600
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNCCTVTPYPS 660
QY 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
DB 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
QY 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
DB 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVTYIILTFVLLNMLTALMGE 720
QY 721 TVGVSKSKSHIWKQ 736
DB 721 TVGVSKSKSHIWKQ 736
QY 721 TVGVSKSKSHIWKQ 736
DB 721 TVGVSKSKSHIWKQ 736

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RESULT 9
US-10-342-844-78
; Sequence 78, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n_1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; FILE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115

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RESULT 10
US-10-415-570A-2
; Sequence 2, Application US/10415570A
; Publication No. US20040198649A1
; GENERAL INFORMATION:
; APPLICANT: Davis, John Beresford

```

; APPLICANT: Gunthorpe, Martin James
 ; APPLICANT: Egeton, Julie
 ; APPLICANT: Smart, Darren
 ; TITLE OF INVENTION: New Use
 ; FILE REFERENCE: P32689
 ; CURRENT APPLICATION NUMBER: US/10/415,570A
 ; PRIOR FILING DATE: 2003-04-23
 ; PRIOR APPLICATION NUMBER: PCT/GB01/04739
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: GB 0026114.9
 ; PRIOR FILING DATE: 2000-10-25
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-415-570A-2

Query Match 99.2%; Score 736; DB 17; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGRAGGAGTAAELPGDESGTGGGAFLSLAULFEGEDGSLSPSPADARPPGP 60
 DB 1 MADSEGRAGGAGTAAELPGDESGTGGGAFLSLAULFEGEDGSLSPSPADARPPGP 60
 QY 61 GDGRPNLBMKFOGAFKGVNPNIDLESTLYESSVVPQKKAAMDLSFDYGYRHHSSDN 120
 DB 61 GDGRPNLBMKFOGAFKGVNPNIDLESTLYESSVVPQKKAAMDLSFDYGYRHHSSDN 120
 QY 121 KRWKRIIEKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRL 180
 DB 121 KRWKRIIEKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRL 180
 QY 121 KRWKRIIEKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRL 180
 DB 121 KRWKRIIEKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRL 180
 QY 181 TDEERESTGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQT 240
 DB 181 TDEERESTGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQT 240
 QY 181 TDEERESTGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQT 240
 DB 181 TDEERESTGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQT 240
 QY 241 ALHAIERCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 300
 DB 241 ALHAIERCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 300
 QY 241 ALHAIERCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 300
 DB 241 ALHAIERCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 300
 QY 301 VNYLTENPKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDS 360
 DB 301 VNYLTENPKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDS 360
 QY 301 VNYLTENPKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDS 360
 DB 301 VNYLTENPKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDS 360
 QY 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYD 420
 DB 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYD 420
 QY 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYD 420
 DB 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYD 420
 QY 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480
 DB 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480
 QY 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480
 DB 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480
 QY 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCGV 540
 DB 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCGV 540
 QY 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCGV 540
 DB 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCGV 540
 QY 541 NSLFLDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
 DB 541 NSLFLDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
 QY 541 NSLFLDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
 DB 541 NSLFLDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
 QY 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCAMKVCNEDQCTVPTYSYC 660
 DB 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCAMKVCNEDQCTVPTYSYC 660
 QY 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCAMKVCNEDQCTVPTYSYC 660
 DB 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCAMKVCNEDQCTVPTYSYC 660
 QY 661 RDSFTSFLLDLFLKLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLTALMGE 720
 DB 661 RDSFTSFLLDLFLKLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLTALMGE 720
 QY 661 RDSFTSFLLDLFLKLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLTALMGE 720
 DB 661 RDSFTSFLLDLFLKLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLTALMGE 720
 QY 721 TVGVSKSKSHIMKLO 736
 DB 721 TVGVSKSKSHIMKLO 736

DB 721 TVGVSKSKSHIMKLO 736

RESULT 11
 US-10-342-844-56
 ; Sequence 56, Application US/10342844
 ; Publication No. US2004009537A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stauderman, Kenneth
 ; APPLICANT: Roos, Jack
 ; APPLICANT: Vellelebi, G'n'l
 ; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
 ; FILE REFERENCE: 37481-3307
 ; CURRENT APPLICATION NUMBER: US/10/342,844
 ; PRIOR FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: US 60/347,459
 ; PRIOR FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: US 60/401,171
 ; PRIOR FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: US 60/405,678
 ; PRIOR FILING DATE: 2002-08-20
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 56
 ; LENGTH: 803
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: Genbank AAK69487
 ; DATABASE ENTRY DATE: 2001-07-02
 US-10-342-844-56

Query Match 90.0%; Score 668; DB 15; Length 803;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 MKFOGAFKGVNPNIDLESTLYESSVVPQKKAAMDLSFDYGYRHHSSDNKRWKRII 128
 DB 1 MKFOGAFKGVNPNIDLESTLYESSVVPQKKAAMDLSFDYGYRHHSSDNKRWKRII 128
 QY 129 EKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRLTDEFRBP 188
 DB 129 EKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRLTDEFRBP 188
 QY 129 EKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRLTDEFRBP 188
 DB 129 EKOPQSKAPAPPPILKVFENRPIFDIVSRGSTADLDGLPFLTHKKRLTDEFRBP 188
 QY 189 STGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQTALHAIER 248
 DB 189 STGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQTALHAIER 248
 QY 189 STGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQTALHAIER 248
 DB 189 STGTCTCPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDIYRQQTALHAIER 248
 QY 249 RCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 308
 DB 249 RCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 308
 QY 249 RCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 308
 DB 249 RCKHYVELLVAOGADVAOARGRFQPKDEGGYFEGELPLSLAECTNOHI 308
 QY 309 HKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDSNLEAVLNN 368
 DB 309 HKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDSNLEAVLNN 368
 QY 309 HKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDSNLEAVLNN 368
 DB 309 HKKADMRQDSRGNTVLAALVAIADNTRENTKVTYKMDLLKCARLPDSNLEAVLNN 368
 QY 369 DGLSPIMMAAATGKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428
 DB 369 DGLSPIMMAAATGKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428
 QY 369 DGLSPIMMAAATGKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428
 DB 369 DGLSPIMMAAATGKIGIFOHIIIRREVDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428
 QY 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488
 DB 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488
 QY 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488
 DB 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488
 QY 489 AAYOPLBGTBPYPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFDIGS 548
 DB 489 AAYOPLBGTBPYPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFDIGS 548
 QY 489 AAYOPLBGTBPYPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFDIGS 548
 DB 489 AAYOPLBGTBPYPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFDIGS 548
 QY 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTGYSIMIQ 608
 DB 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTGYSIMIQ 608
 QY 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTGYSIMIQ 608
 DB 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTGYSIMIQ 608
 QY 481 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTGYSIMIQ 540
 DB 481 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTGYSIMIQ 540

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QY 609 ILFKDLFRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSCRDSETEST 668
DB 541 ILFKDLFRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSCRDSETEST 600
QY 669 FLDDLFKLTIGMDLEMLSTKYVVFILLVTYIIITFVLLNMLALMGSTVQVSKR 728
DB 601 FLDDLFKLTIGMDLEMLSTKYVVFILLVTYIIITFVLLNMLALMGSTVQVSKR 660
QY 729 SKHWKIQ 736
DB 661 SKHWKIQ 668

RESULT 12
US-10-027-828-2
; Sequence 2, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS E
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-828-2

Query Match      85.6%; Score 635; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGEVAVELFGDESGTGGRAFLPSSLANIFEGDGLSPSPADASRPAG 60
DB 1 MADSSGPRAGGEVAVELFGDESGTGGRAFLPSSLANIFEGDGLSPSPADASRPAG 60
QY 61 GGRPVLRMKPGAFKGVNPIDILESTLYESSVVPGRKAPMDSLFDYGYRRHSSDN 120
DB 61 GGRPVLRMKPGAFKGVNPIDILESTLYESSVVPGRKAPMDSLFDYGYRRHSSDN 120
QY 121 KWRKKKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADIDGLPFLTHKKRL 180
DB 121 KWRKKKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADIDGLPFLTHKKRL 180
QY 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
DB 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDGEGYFFGGLPLSLAAGTQPHI 300
DB 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDGEGYFFGGLPLSLAAGTQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVTKMDLLILKCARLPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVTKMDLLILKCARLPDS 360
QY 361 NLEAVIANNDGLSPMLMAAKTKGIGIHOHIIIRREVTDDEDPHLSRKRDMAVGVYSILD 420
DB 361 NLEAVIANNDGLSPMLMAAKTKGIGIHOHIIIRREVTDDEDPHLSRKRDMAVGVYSILD 420
QY 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKGAVSFYINVSYL 480
DB 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKGAVSFYINVSYL 480

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QY 481 ANVIFTLRAYOPLEGTPPYRTTVDIRLAGEVITLFTGLPFTNLIKLEMKKCGV 540
DB 481 ANVIFTLRAYOPLEGTPPYRTTVDIRLAGEVITLFTGLPFTNLIKLEMKKCGV 540
QY 541 NSLFDGSPQLLYFYSVLVYSAALYLAGIRAYAVAWMFALVLMQNALYFRGLKLTG 600
DB 541 NSLFDGSPQLLYFYSVLVYSAALYLAGIRAYAVAWMFALVLMQNALYFRGLKLTG 600
QY 601 TYSIMIQKILFQDLFRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSC 660
DB 601 TYSIMIQKILFQDLFRFLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSC 660
QY 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVVFILLVTYIIITFVLLNMLALMGSE 720
DB 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVVFILLVTYIIITFVLLNMLALMGSE 720
QY 721 TVGVSKSKHWKIQ 736
DB 721 TVGVSKSKHWKIQ 736

RESULT 13
US-10-027-828-4
; Sequence 4, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS E
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-828-4

Query Match      85.6%; Score 635; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGEVAVELFGDESGTGGRAFLPSSLANIFEGDGLSPSPADASRPAG 60
DB 1 MADSSGPRAGGEVAVELFGDESGTGGRAFLPSSLANIFEGDGLSPSPADASRPAG 60
QY 61 GGRPVLRMKPGAFKGVNPIDILESTLYESSVVPGRKAPMDSLFDYGYRRHSSDN 120
DB 61 GGRPVLRMKPGAFKGVNPIDILESTLYESSVVPGRKAPMDSLFDYGYRRHSSDN 120
QY 121 KWRKKKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADIDGLPFLTHKKRL 180
DB 121 KWRKKKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADIDGLPFLTHKKRL 180
QY 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
DB 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDGEGYFFGGLPLSLAAGTQPHI 300
DB 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDGEGYFFGGLPLSLAAGTQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVTKMDLLILKCARLPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVTKMDLLILKCARLPDS 360

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Qy 361 NLEAVLNNDGLSPIMMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAYGPVYSLYD 420
Db 361 NLEAVLNNDGLSPIMMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAYGPVYSLYD 420
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYLIC 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYLIC 480
Qy 481 AMVIFTLTAAYYQPLEGTTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Db 481 AMVIFTLTAAYYQPLEGTTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Qy 541 NSLFDGSPOLLFYFYSVLVISAALYLAGIEAYLAVVFPALVLCMMNALYFTRGKLTG 600
Db 541 NSLFDGSPOLLFYFYSVLVISAALYLAGIEAYLAVVFPALVLCMMNALYFTRGKLTG 600
Qy 601 TYSIMIOKILFKDLFRFLVYLFPWIGYASALVSLINPCANNKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIOKILFKDLFRFLVYLFPWIGYASALVSLINPCANNKVCNEDQNTCTVPTPSC 660
Qy 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
Db 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
Qy 721 TVGVSKESKHIWKIQ 736
Db 721 TVGVSKESKHIWKIQ 736

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RESULT 14

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US-10-090-215-7
; Sequence 7, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
; APPLICANT: Huvair, Arne
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/090,215
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-215-7

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Query Match 85.6%; Score 635; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSSIANLPFGEDGSLSPSPADASRPAGP 60
Db 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSSIANLPFGEDGSLSPSPADASRPAGP 60
Qy 61 GDGRPNLPMKFOGAFRRKGVNPPIDLESTLYESSVVPKAPMDSLFDYGYRHSSDN 120
Db 61 GDGRPNLPMKFOGAFRRKGVNPPIDLESTLYESSVVPKAPMDSLFDYGYRHSSDN 120
Qy 121 KRWKKIIEKOPQSPKAPAPQPPILKVFNRPILEFDIYSGSTADLDGLPFLTHKKRL 180
Db 121 KRWKKIIEKOPQSPKAPAPQPPILKVFNRPILEFDIYSGSTADLDGLPFLTHKKRL 180
Qy 181 TDEFRPSTGCTCLPKALNLSNGRNDTIPVLLDIARTGNMRPFINSPPRIYYRQOT 240
Db 181 TDEFRPSTGCTCLPKALNLSNGRNDTIPVLLDIARTGNMRPFINSPPRIYYRQOT 240
Qy 241 ALHAIERRCKHYVELLVAOGADYVAOARGFPQPKDGGYFYFGEELPLSLAACNQH 300
Db 241 ALHAIERRCKHYVELLVAOGADYVAOARGFPQPKDGGYFYFGEELPLSLAACNQH 300

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Db 241 ALHAIERRCKHYVELLVAOGADYVAOARGFPQPKDGGYFYFGEELPLSLAACNQH 300
Qy 301 VNYLTENPHKKADMRQDSRGNTVLAHVAIADNTRNTKFTYKAYDILLKCARLPDPS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLAHVAIADNTRNTKFTYKAYDILLKCARLPDPS 360
Qy 361 NLEAVLNNDGLSPIMMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAYGPVYSLYD 420
Db 361 NLEAVLNNDGLSPIMMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAYGPVYSLYD 420
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYLIC 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYLIC 480
Qy 481 AMVIFTLTAAYYQPLEGTTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Db 481 AMVIFTLTAAYYQPLEGTTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Qy 541 NSLFDGSPOLLFYFYSVLVISAALYLAGIEAYLAVVFPALVLCMMNALYFTRGKLTG 600
Db 541 NSLFDGSPOLLFYFYSVLVISAALYLAGIEAYLAVVFPALVLCMMNALYFTRGKLTG 600
Qy 601 TYSIMIOKILFKDLFRFLVYLFPWIGYASALVSLINPCANNKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIOKILFKDLFRFLVYLFPWIGYASALVSLINPCANNKVCNEDQNTCTVPTPSC 660
Qy 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
Db 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
Qy 721 TVGVSKESKHIWKIQ 736
Db 721 TVGVSKESKHIWKIQ 736

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RESULT 15

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US-10-342-844-60
; Sequence 60, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, Gyn_1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAG28029
; DATABASE ENTRY DATE: 2000-10-31
US-10-342-844-60

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Query Match 85.6%; Score 635; DB 15; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSSIANLPFGEDGSLSPSPADASRPAGP 60
Db 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSSIANLPFGEDGSLSPSPADASRPAGP 60

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QY 61 GGRPNLAKMKFOGAPRKGVNPIDILESTLYESSVVPGEKAPMDSLFDYGYRRHSSDN 120
Db 61 GGRPNLAKMKFOGAPRKGVNPIDILESTLYESSVVPGEKAPMDSLFDYGYRRHSSDN 120
QY 121 KWRKKIIEKOPQSPKAPAPQPPPIIKVNNRPIIFDIVSGSTADIDGLPLPLTHKKRL 180
Db 121 KWRKKIIEKOPQSPKAPAPQPPPIIKVNNRPIIFDIVSGSTADIDGLPLPLTHKKRL 180
QY 181 TDEEPEPESTGTCCLPKALINTSNGRNDTIPVLIDIAERTGNMREPTNSPPRDIYYRGOT 240
Db 181 TDEEPEPESTGTCCLPKALINTSNGRNDTIPVLIDIAERTGNMREPTNSPPRDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGYYFYFGEPLPLSLAAGTNPPI 300
Db 241 ALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGYYFYFGEPLPLSLAAGTNPPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDLILLCARLPDS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDLILLCARLPDS 360
QY 361 NLEAVLNNDGLSPIMAAKTKIGIFQHTIRREVTDETRHLSRKFCDWAGPVYSSLYD 420
Db 361 NLEAVLNNDGLSPIMAAKTKIGIFQHTIRREVTDETRHLSRKFCDWAGPVYSSLYD 420
QY 421 LSSLDTGCEEASVLEILVYNSKIENHEMLAVEPINELDRKMKFGAVSYINVSYLQ 480
Db 421 LSSLDTGCEEASVLEILVYNSKIENHEMLAVEPINELDRKMKFGAVSYINVSYLQ 480
QY 481 AMVIFLTLAYYQBLEGTPPYPTTYDYLRLAGEVITLFTGYLFFFTNFKDLFMKCPGV 540
Db 481 AMVIFLTLAYYQBLEGTPPYPTTYDYLRLAGEVITLFTGYLFFFTNFKDLFMKCPGV 540
QY 541 NSLFDGSPQLYFYISVIVISAALYLAGIEAYLAVMTFALVGMNNAIYFTRGKLTG 600
Db 541 NSLFDGSPQLYFYISVIVISAALYLAGIEAYLAVMTFALVGMNNAIYFTRGKLTG 600
QY 601 TYSIMIOKILFKDLFRFLLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
Db 601 TYSIMIOKILFKDLFRFLLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
QY 661 RDESESTFLDLFKLTIGMDLEMLSSTKYPVVFIIILVTYIILFVLLINMLIALMGB 720
Db 661 RDESESTFLDLFKLTIGMDLEMLSSTKYPVVFIIILVTYIILFVLLINMLIALMGB 720
QY 721 TVGQVSKESKHITKQ 736
Db 721 TVGQVSKESKHITKQ 736
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Job time : 151 secs